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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 28.1194 Seconds
(without alignments)
120.578 Million cell updates/sec

Title: US-09-641-802-4
Perfect score: 62
Sequence: 1 LFFFPLPVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	62	100.0	12	4	AAB72503	Aab72503 Colostrin
2	62	100.0	12	4	AAB59323	Aab59323 Ewe colos
3	62	100.0	12	4	AAB72249	Aab72249 Colostrin
4	62	100.0	12	4	AAB72535	Aab72535 Colostrin
5	62	100.0	12	5	AAO14580	Aao14580 Neural ce
6	62	100.0	12	5	AAM51039	Aam51039 Colostrin
7	62	100.0	12	5	AAE20231	Aae20231 Colostrin
8	62	100.0	14	4	AAB59353	Aab59353 Ewe colos
9	35	56.5	14	4	AAM96786	Aam96786 Human pep

10	33	53.2	9	2	AAY21194	Aay21194 Human bcl
11	31	50.0	7	4	AAE07196	Aae07196 Modified
12	31	50.0	9	6	ABP75278	Abp75278 Chlamydia
13	31	50.0	18	2	AAY12581	Aay12581 Human 5'
14	30	48.4	13	6	ABU07592	Abu07592 FIPV 1B p
15	30	48.4	15	6	ABP68061	Abp68061 Bacillus
16	29	46.8	9	3	AAG61675	Aag61675 Arabidops
17	29	46.8	9	6	ABP75371	Abp75371 Chlamydia
18	29	46.8	10	5	ABJ01746	Abj01746 158P1D7 r
19	29	46.8	11	2	AAW69637	Aaw69637 Peptide S
20	29	46.8	11	2	AAW74434	Aaw74434 Ste2 agon
21	29	46.8	11	3	AAY93630	Aay93630 Peptide e
22	29	46.8	11	3	AAB20744	Aab20744 MF-alpha-
23	29	46.8	11	4	AAG79162	Aag79162 Amino aci
24	29	46.8	11	4	AAB84510	Aab84510 Amino aci
25	29	46.8	11	6	ABU10264	Abu10264 Alpha-fac
26	29	46.8	13	4	AAB45712	Aab45712 Human 7TM
27	29	46.8	14	5	ABG67849	Abg67849 Human ADP
28	29	46.8	14	6	ADA24208	Ada24208 Alzheimer
29	29	46.8	14	6	ADA23994	Ada23994 Alzheimer
30	29	46.8	14	6	ADA23993	Ada23993 Alzheimer
31	29	46.8	18	4	AAB89134	Aab89134 HIV gp120
32	29	46.8	18	4	AAB89135	Aab89135 HIV gp120
33	29	46.8	18	6	ABJ37110	Abj37110 Concatame
34	28	45.2	8	2	AAW81861	Aaw81861 Human pro
35	28	45.2	9	6	ABP75281	Abp75281 Chlamydia
36	28	45.2	9	6	ABP75273	Abp75273 Chlamydia
37	28	45.2	15	4	AAG64341	Aag64341 Ribosomal
38	27	43.5	9	3	AAB23686	Aab23686 Cytotoxic
39	27	43.5	9	5	ABG79052	Abg79052 Human Gpl
40	27	43.5	9	5	AAO17100	Aao17100 Human gp1
41	27	43.5	9	5	ABG66788	Abg66788 Tumour an
42	27	43.5	10	6	ABJ19645	Abj19645 Neuronal
43	27	43.5	11	3	AAY93625	Aay93625 Peptide a
44	27	43.5	14	5	AAU09823	Aau09823 Modified
45	27	43.5	15	3	AAY98981	Aay98981 HLA class
46	27	43.5	15	4	AAG84564	Aag84564 MAGE2 DR
47	27	43.5	15	4	AAG84573	Aag84573 MAGE2 DR
48	27	43.5	15	4	AAG84885	Aag84885 MAGE2 DR3
49	27	43.5	15	4	AAG84649	Aag84649 MAGE2 DR
50	27	43.5	17	2	AAY21126	Aay21126 Human bcl
51	27	43.5	18	2	AAW65655	Aaw65655 Peptide #
52	27	43.5	18	4	AAO05419	Aao05419 Human pol
53	26	41.9	9	6	ABJ20116	Abj20116 MHC bindi
54	26	41.9	9	6	ABP75365	Abp75365 Chlamydia
55	26	41.9	9	6	ABP75379	Abp75379 Chlamydia
56	26	41.9	10	3	AAY57312	Aay57312 P. aerugi
57	26	41.9	10	4	AAG94915	Aag94915 Human com
58	26	41.9	10	5	ABJ01803	Abj01803 158P1D7 r
59	26	41.9	10	5	ABJ01727	Abj01727 158P1D7 r
60	26	41.9	10	5	ABJ01913	Abj01913 158P1D7 r
61	26	41.9	12	3	AAY69453	Aay69453 Antimicro
62	26	41.9	13	3	AAY69461	Aay69461 Antimicro
63	26	41.9	14	4	AAM98289	Aam98289 Human pep
64	26	41.9	14	4	AAM98290	Aam98290 Human pep
65	26	41.9	14	7	ADC17436	Adc17436 Type IV c
66	26	41.9	15	4	AAG66435	Aag66435 Human spl

67	26	41.9	15	5	ABP55519	Abp55519 Human tra
68	26	41.9	15	5	AAM47974	Aam47974 Human cyt
69	26	41.9	15	5	AAM47998	Aam47998 Human RNA
70	26	41.9	15	6	ABP59886	Abp59886 Human neu
71	26	41.9	16	2	AAR33427	Aar33427 NADH:FMN
72	26	41.9	16	3	AAY88502	Aay88502 Peptide #
73	26	41.9	17	4	AAE01592	Aae01592 Human gen
74	26	41.9	17	5	ABG63823	Abg63823 Human alb
75	26	41.9	18	3	AAY77534	Aay77534 Winter wh
76	26	41.9	18	4	AAB89133	Aab89133 HIV gp120
77	25	40.3	11	6	AAE32247	Aae32247 Arabidops
78	25	40.3	11	6	ABP68032	Abp68032 Bacillus
79	25	40.3	12	2	AAW69842	Aaw69842 Peptide f
80	25	40.3	12	5	AAU09822	Aau09822 Modified
81	25	40.3	13	2	AAY41944	Aay41944 Rheumatoi
82	25	40.3	13	2	AAW93225	Aaw93225 Human cyt
83	25	40.3	13	4	ABB52107	Abb52107 Human API
84	25	40.3	13	6	ABR58950	Abr58950 Alzheimer
85	25	40.3	14	4	AAU69184	Aau69184 Human Ace
86	25	40.3	14	7	ABR42944	Abr42944 Human exo
87	25	40.3	15	2	AAW89741	Aaw89741 Human C-r
88	25	40.3	15	4	AAG64438	Aag64438 Human RCC
89	25	40.3	16	5	ABP46239	Abp46239 Human BLY
90	25	40.3	17	4	AAB61244	Aab61244 Gerbil TA
91	25	40.3	17	6	ABO32680	Abo32680 Secreted
92	25	40.3	17	7	ADB90790	Adb90790 Gerbil TA
93	25	40.3	18	2	AAW45179	Aaw45179 C-reactiv
94	25	40.3	18	3	AAY65312	Aay65312 Human 5'
95	25	40.3	18	4	AAB98389	Aab98389 SCF prote
96	25	40.3	18	4	AAB98390	Aab98390 SCF prote
97	25	40.3	18	4	AAU02480	Aau02480 Human C-t
98	25	40.3	18	4	AAU02481	Aau02481 Human C-t
99	25	40.3	18	4	AAB96974	Aab96974 Mammalian
100	25	40.3	18	4	AAB96975	Aab96975 Mammalian

ALIGNMENTS

RESULT 1

AAB72503

ID AAB72503 standard; peptide; 12 AA.

XX

AC AAB72503;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #4.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.
XX
PR 17-AUG-1999; 99US-0149310P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the cell with an oxidative stress regulator selected from colostrinin, its constituent peptide, analog or their combinations.
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative stress level in a cell or a patient, comprising contacting the cell with, or administering to the patient, an oxidative stress regulator selected from colostrinin, or its constituent peptide (e.g. the present peptide), to change the level of an oxidising species in the cell. The method can be used to treat oxidative damage to skin, by decreasing or preventing an increase in the level of damage to a biomolecule of the patient
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
||| ||| ||| |||
Db 1 LFFF LPVV NVLP 12

RESULT 2
AAB59323
ID AAB59323 standard; peptide; 12 AA.
XX
AC AAB59323;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment B-8.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder; central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB002128.
XX
PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
Db 1 LFFF LPVV NVLP 12

RESULT 3
AAB72249
ID AAB72249 standard; peptide; 12 AA.
XX
AC AAB72249;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 4.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022818.
XX

PR 17-AUG-1999; 99US-0149311P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator.
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The peptides
CC have immune response modulatory activity, and are capable of inducing
CC cytokines. Colostrinin and its derived peptides are useful for inducing
CC cytokine production, for modulating an immunological response and for
CC inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVL P 12
||| ||| ||| |||
Db 1 LFFF LPVV NVL P 12

RESULT 4
AAB72535
ID AAB72535 standard; peptide; 12 AA.
XX
AC AAB72535;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #4.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.

XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
| | | | | | | | | | | |
Db 1 LFFF LPVV NVLP 12

RESULT 5
AAO14580
ID AAO14580 standard; peptide; 12 AA.
XX
AC AAO14580;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 4.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX

PF 17-AUG-2000; 2000WO-US022777.
XX
PR 17-AUG-2000; 2000WO-US022777.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell regulator selected from colostrinin, its constituent peptide and/or analog.
XX
PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g. neural cell differentiation). The method involves contacting cells with a neural cell regulator (i.e. a colostrinin peptide) in order to change the cells in morphology to form neural cells. Colostrinin is a proline-rich polypeptide aggregate that is present in colostrum. The method of the invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
||| ||| ||| |||
Db 1 LFFF LPVV NVLP 12

RESULT 6
AAM51039
ID AAM51039 standard; peptide; 12 AA.
XX
AC AAM51039;
XX
DT 30-MAY-2002 (first entry)
XX
DE Colostrinin constituent peptide.
XX
KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "optional C-terminal amidation"
XX
PN WO200213849-A1.

XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022775.
XX
PR 17-AUG-2000; 2000WO-US022775.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
DR WPI; 2002-269150/31.
XX
PT Modulation of blood cell proliferation in a patient involves use of blood
PT cell regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 1; Page 34; 54pp; English.
XX
CC The present sequence is that of a colostrinin constituent peptide that is
CC preferred for use as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. It is classified as having
CC a beta-casein homologue precursor. Methods are claimed for: inducing a
CC cytokine in a cell by contact with an immunological regulator, where the
CC cell is present in a cell culture, a tissue, an organ or an organism, and
CC the cell is mammalian, including human; modulating an immune response in
CC a cell by contact with the immunological regulator under conditions
CC effective to induce a cytokine; modulating an immune response in a
CC patient by administering an immunological regulator under conditions
CC effective to induce a cytokine, where the immunological regulator is
CC administered topically or as part of a dietary supplement, and where the
CC immune response is specific or non specific, an interferon response or an
CC antibody response; modulating blood cell proliferation by contacting
CC blood cells with a blood cell regulator, where the blood cells are
CC present in a cell culture or an organism, are mammalian or human, and
CC where the blood cells are increased in number or differentiated; and a
CC method for modulating blood cell proliferation in a patient. A claimed
CC cytokine-inducing composition comprises a pharmaceutical carrier and an
CC active agent such as the present peptide. Cytokines induced by this
CC peptide in human leucocyte cultures include interferon-gamma, tumour
CC necrosis factor-alpha, interleukin-6 and interleukin-10
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFLPVVNVL 12
||| ||| ||| |||
Db 1 LFFFLPVVNVL 12

RESULT 7
AAE20231
ID AAE20231 standard; peptide; 12 AA.

XX
AC AAE20231;
XX
DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #4.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "Optionally C-terminal amide"
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US022776.
XX
PR 17-AUG-2000; 2000WO-US022776.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.
XX
PS Claim 6; Page 25; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
| | | | | | | | | | | |
Db 1 LFFF LPVV NVLP 12

RESULT 8

AAB59353

ID AAB59353 standard; peptide; 14 AA.

XX

AC AAB59353;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #13.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 62; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVLP 12
||| ||| ||| |||
Db 2 LFFF LPVV NVLP 13

RESULT 9
AAM96786
ID AAM96786 standard; peptide; 14 AA.
XX
AC AAM96786;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #61 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3681; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,

CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX

SQ Sequence 14 AA;

Query Match 56.5%; Score 35; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPVVNV 10
|: :|||||
Db 2 FYVMPVVNV 10

RESULT 10

AAY21194

ID AAY21194 standard; protein; 9 AA.

XX

AC AAY21194;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human bcl2 proto-oncogene mutant protein fragment 42.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75766.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
PS Disclosure; Fig 15; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC use of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGPC) and neuroendocrine specific protein A
XX
SQ Sequence 9 AA;

Query Match 53.2%; Score 33; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
Db 4 FFFLPV 9

RESULT 11
AAE07196
ID AAE07196 standard; peptide; 7 AA.
XX
AC AAE07196;
XX
DT 06-NOV-2001 (first entry)
XX
DE Modified colostrinin cyclic peptide #2.
XX
KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;

KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic
FT linkage with Asn found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the
PT immune system and the central nervous system comprises ten amino-terminal
PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Example 2; Page 8; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxillary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child. The
CC present sequence is modified colostrinin cyclic peptide #2 related to the
CC invention

XX

SQ Sequence 7 AA;

Query Match 50.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVFN 9
|||||
Db 2 FLPVFN 7

RESULT 12
ABP75278
ID ABP75278 standard; peptide; 9 AA.
XX
AC ABP75278;
XX
DT 20-FEB-2003 (first entry)
XX
DE Chlamydia pneumonia peptide epitope #44.
XX
KW Antibacterial; secreted protein; intracellular bacterium.
XX
OS Chlamydia pneumonia.
XX
PN WO200282091-A2.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002WO-DK000234.
XX
PR 09-APR-2001; 2001DK-00000581.
PR 09-APR-2001; 2001US-0282513P.
XX
PA (SHAW//) SHAW A C.
PA (VAND//) VANDAHL B B.
XX
PI Shaw AC, Vandahl BB;
XX
DR WPI; 2003-058585/05.
XX
PT Identifying intracellular bacterial proteins by labeling proteins in the
PT presence of a eukaryotic protein synthesis inhibitor, performing
PT electrophoresis, autoradiography and comparing profiles to an infected-
PT cell lysate profile.
XX
PS Claim 34; Page 145; 179pp; English.
XX
CC The present invention relates to a method (M1) for identifying secreted
CC intracellular bacterial proteins (BP). M1 comprises: (a) selectively
CC visualising BP by pulse labelling in the presence of an inhibitor of
CC eukaryotic protein synthesis followed by 2D electrophoresis and
CC autoradiography; (b) comparing protein profiles (PF) of purified bacteria
CC to PF of total lysate (TL) of infected cells; and (c) identifying protein
CC spots present in differential images from gels loaded with TL. The
CC present sequence is one such bacterial peptide epitope which was
CC identified by the method of the invention
XX
SQ Sequence 9 AA;

Query Match 50.0%; Score 31; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFFFLPVV 8
|| |||:
Db 2 LFTFLPII 9

RESULT 13

AAY12581

ID AAY12581 standard; protein; 18 AA.

XX

AC AAY12581;

XX

DT 22-JUN-1999 (first entry)

XX

DE Human 5' EST secreted protein SEQ ID NO: 246 from WO 9906553.

XX

KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; antiinflammatory; tumour inhibition; antitumour.

XX

OS Homo sapiens.

XX

PN WO9906553-A2.

XX

PD 11-FEB-1999.

XX

PF 31-JUL-1998; 98WO-IB001237.

XX

PR 01-AUG-1997; 97US-00905051.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Lacroix B;

XX

DR WPI; 1999-153783/13.

DR N-PSDB; AAX41439.

XX

PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries derived from umbilical cord, lymph ganglia, lymphocytes and
PT placental tissue.

XX

PS Claim 34; Page 357; 411pp; English.

XX

CC AAX41379 to AAX41526 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12521 to
CC AAY12668, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ ligand activity, antiinflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX

SQ Sequence 18 AA;

Query Match 50.0%; Score 31; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFFILPVV 8
|| |:|||
Db 6 LFCFMPVV 13

RESULT 14

ABU07592

ID ABU07592 standard; peptide; 13 AA.

XX

AC ABU07592;

XX

DT 27-MAR-2003 (first entry)

XX

DE FIPV 1B protein C-terminus from pBDRI2.

XX

KW pBRDI2; virucide; antibacterial; antiparasitic; VLP; virus-like particle;
KW coronavirus; attenuated virus; structural protein; nucleocapsid protein;
KW membrane protein; envelope protein; spike protein; immunogen; vaccine;
KW luciferase; haemagglutinin esterase; FIPV.

XX

OS Feline infectious peritonitis virus.

XX

PN WO200292827-A2.

XX

PD 21-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-NL000318.

XX

PR 17-MAY-2001; 2001EP-00201861.

XX

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX

PI Rottier PJM, De Haan CAM, Hajema BJ, Bosch BJ;

XX

DR WPI; 2003-120691/11.

DR N-PSDB; ABX15612.

XX

PT Novel isolated or recombinant virus-like particle derived from
PT coronavirus for therapeutic and diagnostic purposes, and as immunogen or
PT vaccine, has functionally deleted fragments and is capable of
PT replication.

XX

PS Disclosure; Fig 14; 138pp; English.

XX

CC The invention relates to isolated or recombinant virus-like particle
CC (VLP) capable of replication, derived from coronavirus (e.g. mouse
CC hepatitis virus, MHV), having functionally deleted genomes. The
CC functional fragment from nucleic acid encoding viral gene product other
CC than polymerase or structural protein (SP) like nucleocapsid (N),
CC membrane (M), envelope (E) or spike (S) protein, is deleted, or genes for
CC SP do not occur in the order 5'-S-E-M-N-3'. Also included are a
CC composition comprising the VLP, and a carrier for therapeutic and
CC diagnostic use, as an immunogen or vaccine and inhibiting or blocking an
CC infection with a coronavirus or corona-VLP, by treating an organism with
CC a heptad repeat peptide or its functional fragment. The VLP composition
CC is useful for therapeutic and diagnostic purposes, and as an immunogen or
CC vaccine. The VLP is also useful as gene delivery vehicle, and for
CC eliciting immune response against proteins e.g. viral, bacterial,
CC parasitic, and cellular origins. Attenuated feline infectious peritonitis
CC virus (FIPV) VLPs were constructed expressing Renilla luciferase referred
CC to as pBRDI2. The present sequence is FIPV 1B protein C-terminus from
CC pBRDI2

XX

SQ Sequence 13 AA;

Query Match 48.4%; Score 30; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFFPLPVV 8
||:| |:
Db 6 LFYFCPLV 13

RESULT 15

ABP68061

ID ABP68061 standard; peptide; 15 AA.

XX

AC ABP68061;

XX

DT 08-JAN-2003 (first entry)

XX

DE Bacillus thuringiensis toxin Cry related peptide #28.

XX

KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.

XX

OS Bacillus thuringiensis.

OS Synthetic.

XX

PN FR2822157-A1.

XX

PD 20-SEP-2002.

XX

PF 19-MAR-2001; 2001FR-00003691.

XX

PR 19-MAR-2001; 2001FR-00003691.

XX

PA (AVET) AVENTIS CROPSCIENCE SA.

XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 3; Page 28; 134pp; French.
XX
CC The present invention describes a modified Cry protein (I) that is sensitive to pepsin and comprises at least one additional pepsin cleavage site (PCS). Also described: (a) increasing pepsin sensitivity of Cry proteins by incorporating at least one extra PCS; (b) polynucleotides (II) that encode (I); (c) chimeric genes (CG) that contain a promoter, (II) and terminator; (d) expression or transformation vector (III) that contains CG; (e) host organism (IV) transformed with (III), also, where the organism is a plant, its parts and seeds; (f) production of (I) by growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed against (I). (I) has insecticide activity. (I) can be used as insecticides, particularly where expressed in transgenic plants. (I) are sensitive to enzymes in the digestive tract of mammals, so do not persist in the tract (lack of persistence is required by regulatory authorities for use, in foods, of seeds containing Cry proteins). Extra PCS do not increase degradation in the digestive tract of insects, so have no effect on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308 represent sequences used in the exemplification of the present invention
XX
SQ Sequence 15 AA;

Query Match 48.4%; Score 30; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLPVNV 10
|||:|||
Db 8 FFLPLLSV 15

RESULT 16
AAG61675
ID AAG61675 standard; protein; 9 AA.
XX
AC AAG61675;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80031.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.

PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 46.8%; Score 29; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| | | | |
Db 1 FFFLP 5

RESULT 17
ABP75371
ID ABP75371 standard; peptide; 9 AA.
XX
AC ABP75371;
XX
DT 20-FEB-2003 (first entry)
XX
DE Chlamydia trachomatis peptide epitope #77.
XX
KW Antibacterial; secreted protein; intracellular bacterium.
XX
OS Chlamydia trachomatis.
XX
PN WO200282091-A2.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002WO-DK000234.
XX
PR 09-APR-2001; 2001DK-00000581.
PR 09-APR-2001; 2001US-0282513P.
XX
PA (SHAW/) SHAW A C.
PA (VAND/) VANDAHL B B.
XX
PI Shaw AC, Vandahl BB;
XX
DR WPI; 2003-058585/05.
XX
PT Identifying intracellular bacterial proteins by labeling proteins in the
PT presence of a eukaryotic protein synthesis inhibitor, performing
PT electrophoresis, autoradiography and comparing profiles to an infected-
PT cell lysate profile.

XX
PS Claim 54; Page 175; 179pp; English.
XX
CC The present invention relates to a method (M1) for identifying secreted
CC intracellular bacterial proteins (BP). M1 comprises: (a) selectively
CC visualising BP by pulse labelling in the presence of an inhibitor of
CC eukaryotic protein synthesis followed by 2D electrophoresis and
CC autoradiography; (b) comparing protein profiles (PF) of purified bacteria
CC to PF of total lysate (TL) of infected cells; and (c) identifying protein
CC spots present in differential images from gels loaded with TL. The
CC present sequence is one such bacterial peptide epitope which was
CC identified by the method of the invention
XX

SQ Sequence 9 AA;

Query Match 46.8%; Score 29; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFFLPVV 8
|| |:|:::
Db 2 LFTFMPPI 9

RESULT 18
ABJ01746
ID ABJ01746 standard; peptide; 10 AA.
XX
AC ABJ01746;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158P1D7 related HLA peptide SEQ ID No 446.
XX
KW Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
PN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026276.
XX
PR 22-AUG-2000; 2000US-0227098P.
PR 10-APR-2001; 2001US-0282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Challita-Eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158P1D7), its encoded

PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses or
PT humans).

XX

PS Disclosure; Page 142; 181pp; English.

XX

CC The invention relates to a novel nucleic acid, designated 158P1D7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158P1D7 protein of the invention

XX

SQ Sequence 10 AA;

Query Match 46.8%; Score 29; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFFLPVVNVL 11
| ||| |:
Db 1 FTHLPVSNIL 10

RESULT 19

AAW69637

ID AAW69637 standard; peptide; 11 AA.

XX

AC AAW69637;

XX

DT 19-OCT-1998 (first entry)

XX

DE Peptide SEQ ID NO:57 from US5789184 Example 5.

XX

KW Yeast; *Saccharomyces cerevisiae*; pheromone; alpha factor; receptor;
KW surrogate; screening; selection.

XX

OS Synthetic.

XX

PN US5789184-A.

XX

PD 04-AUG-1998.

XX

PF 05-JUN-1995; 95US-00464531.

XX

PR 31-MAR-1993; 93US-00041431.

PR 31-JAN-1994; 94US-00190328.

PR 20-SEP-1994; 94US-00309313.

PR 13-OCT-1994; 94US-00322137.

XX

PA (CADU-) CADUS PHARM CORP.

XX

PI Manfredi J, Murphy AJ, Fowlkes DM, Trueheart J, Klein C, Paul J;

PI Broach J;

XX

DR WPI; 1998-446076/38.
DR N-PSDB; AAV50008.

XX
PT Recombinant yeast cells - containing gene encoding yeast pheromone system
PT protein surrogate and gene encoding peptide modulator.

XX
PS Example 5; Col 125; 93pp; English.

XX
CC The present invention describes a yeast cell having a pheromone system,
CC in which the cell comprises: (a) a first heterologous gene encoding a
CC heterologous surrogate of a yeast pheromone system protein, the surrogate
CC being a kinase and performing in the pheromone system of the yeast cell a
CC function naturally performed by the corresponding yeast pheromone system
CC protein; and (b) a second heterologous gene encoding a heterologous
CC peptide, where the heterologous peptide modulates the interaction of the
CC surrogate with the pheromone system in the yeast cell, and the modulation
CC is a selectable or screenable event. The yeast cells are used in assaying
CC a peptide for modulation of the activity of a non- yeast surrogate for a
CC pheromone system protein and determining by detecting a change in the
CC selectable or screenable event whether the pheromone signal pathway is
CC activated or inhibited by the interaction of the surrogate and the
CC peptide. The present sequence represents a peptide which is used in an
CC example of the present invention

XX
SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||
Db 6 FFFLP 10

RESULT 20
AAW74434
ID AAW74434 standard; peptide; 11 AA.

XX
AC AAW74434;

XX
DT 20-MAR-2003 (revised)
DT 10-MAY-1999 (first entry)

XX
DE Ste2 agonist peptide sequence.

XX
KW Yeast pheromone; Ste2 agonist; cognate yeast pheromone system protein;
KW farnesyl transferase; anticancer therapy.

XX
OS Synthetic.

XX
PN US5876951-A.

XX
PD 02-MAR-1999.

XX
PF 05-JUN-1995; 95US-00461598.

XX

PR 31-MAR-1993; 93US-00041431.
PR 31-JAN-1994; 94US-00190328.
PR 20-SEP-1994; 94US-00309313.
PR 13-OCT-1994; 94US-00322137.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Manfredi J, Murphy AJ, Fowlkes DM, Trueheart J, Klein C, Paul J;
PI Broach J;
XX
DR WPI; 1999-189631/16.
DR N-PSDB; AAX18224.
XX
PT Yeast cells having an engineered pheromone system - useful for
PT identifying drugs which can inhibit or activate pheromone system protein,
PT e.g. to develop anti-cancer therapies.
XX
PS Example 5; Col 61; 93pp; English.
XX
CC This sequence represents an Ste2 agonist peptide sequence. The invention
CC relates to Yeast cells engineered to express an exogenous protein capable
CC of substituting for a yeast protein involved in the post-translational
CC modification, transport, recognition or signal transduction of a yeast
CC pheromone. The system can be used to identify drugs which inhibit or
CC activate the ability of the surrogate to substitute for the cognate yeast
CC pheromone system protein. Inhibitors of farnesyl transferase identified
CC can be used for anticancer therapies. (Updated on 20-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| || ||
Db 6 FFFLP 10

RESULT 21
AAY93630
ID AAY93630 standard; peptide; 11 AA.
XX
AC AAY93630;
XX
DT 25-SEP-2000 (first entry)
XX
DE Peptide encoded by the insert of an a-factor variant.
XX
KW Surrogate ligand; formyl peptide receptor like-1 receptor;
KW FPRL-1 receptor; signal transduction; cellular receptor; a-factor;
KW ABC transporter; ion channel.
XX
OS Synthetic.
XX
PN WO200031261-A2.

XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US027909.
XX
PR 25-NOV-1998; 98US-0109902P.
PR 30-NOV-1998; 98US-00201396.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Klein CA, Murphy AJ, Paul J;
XX
DR WPI; 2000-400071/34.
XX
PT Recombinant cell used to identify modulators of heterologous formyl peptide receptor like-1 (FPRL-1) receptor, comprising FPRL-1 receptor expressed in the cell membrane, and a FPRL-1 receptor ligand agonist.
XX
PS Example 5; Page 88; 156pp; English.
XX
CC AAY93628-31 represent peptides encoded by the inserts of a-factor variants identified from random peptide libraries. These variants have utility as improved substrates of ABC transporters expressed in yeast. The specification describes a method for screening and identifying pharmaceutically effective compounds which specifically interact with and modulate the activity of a cellular receptor or ion channel. The method uses a cells which expresses a heterologous formyl peptide receptor like-1 (FPRL-1) receptor in the cell membrane, so that extracellular signal interaction with the receptors extracellular region modulates signal transduction via the receptor. The cell is used in a method to screen and identify pharmaceutically effective compounds which specifically interact with and modulate the activity of a cellular receptor or ion channel, especially the FPRL-1 receptor
XX
SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||
Db 6 FFFLP 10

RESULT 22
AAB20744
ID AAB20744 standard; peptide; 11 AA.
XX
AC AAB20744;
XX
DT 21-DEC-2000 (first entry)
XX
DE MF-alpha-1 expression construct peptide SEQ ID NO:57.
XX
KW Yeast; pheromone; alpha-factor; transporter; pheromone receptor;
KW G alpha subunit; MF alpha 1; MFal; STE2; STE3; C5a receptor; GPA1;

KW G protein coupled receptor; mutagenesis; amplification; screening;
KW hybrid; agonist; antagonist; signal transduction; detection;
KW identification.

XX

OS *Saccharomyces cerevisiae*.
OS Synthetic.

XX

PN US6100042-A.

XX

PD 08-AUG-2000.

XX

PF 13-OCT-1994; 94US-00322137.

XX

PR 31-MAR-1993; 93US-00041431.

PR 31-JAN-1994; 94US-00190328.

PR 20-SEP-1994; 94US-00309313.

XX

PA (CADU-) CADUS PHARM CORP.

XX

PI Fowlkes DM, Broach J, Klein C, Murphy AJ, Paul J, Trueheart J;
PI Manfredi J;

XX

DR WPI; 2000-531665/48.

XX

PT Mixture of recombinant yeast cells comprising a heterologous G protein
PT coupled receptor whose signal transduction activity is modulated by a
PT heterologous polypeptide which provides a detectable signal on
PT modulation.

XX

PS Example 5; Col 63; 95pp; English.

XX

CC The present invention describes recombinant yeast cell mixtures (I). Each
CC (I) has a heterologous G protein coupled receptor (GPCR) expressed in the
CC cell membrane such that signal transduction (ST) activity via GPCR is
CC modulated by interaction of extracellular region (ER) of GPCR with a
CC heterologous polypeptide (P) which interacts with ER of receptor.
CC Modulation of the ST activity by (P) provides a detectable signal. Also
CC described is a recombinant yeast cell (II) that has a cell membrane which
CC comprises a GPCR such that ST activity via GPCR is modulated by
CC interaction of an ER of GPCR with an extracellular signal, and a (P)
CC which is transported to a location allowing interaction with ER of GPCR.
CC (I) is used for identifying a modulator of (P) expressed by the yeast
CC cell which involves providing (I) which comprises heterologous GPCR and a
CC heterologous test polypeptide, allowing the cells within the mixture to
CC generate a detectable signal and then identifying the heterologous test
CC peptide as a modulator of the heterologous receptor protein expressed by
CC the yeast cell. The yeast cells may be used to identify drugs which
CC inhibit or activate, to a detectable degree, the ability of the surrogate
CC to substitute for the cognate yeast pheromone system proteins. The yeast
CC cell is also used to screen agonists and antagonists. The present
CC sequence is used in the exemplification of the present invention

XX

SQ Sequence 11 AA;

Query Match 46.88; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| | | |
Db 6 FFFLP 10

RESULT 23
AAG79162
ID AAG79162 standard; peptide; 11 AA.
XX
AC AAG79162;
XX
DT 03-JAN-2002 (first entry)
XX
DE Amino acid sequence of an improved a-factor variant.
XX
KW Cellular receptor; ion channel; cellular activity; drug discovery;
KW orphan receptor ligand; a-factor; ABC transporter.
XX
OS Synthetic.
XX
PN US2001026926-A1.
XX
PD 04-OCT-2001.
XX
PF 21-DEC-2000; 2000US-00747774.
XX
PR 31-MAR-1993; 93US-00041431.
PR 31-JAN-1994; 94US-00190328.
PR 20-SEP-1994; 94US-00309313.
PR 13-OCT-1994; 94US-00322137.
PR 05-JUN-1995; 95US-00461383.
PR 05-JUN-1995; 95US-00461598.
PR 05-JUN-1995; 95US-00463181.
PR 05-JUN-1995; 95US-00464531.
PR 17-JAN-1996; 96US-00582333.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Klein CA, Murphy AJ, Fowlkes DM, Broach J, Manfredi J, Paul J;
PI Trueheart J;
XX
DR WPI; 2001-615870/71.
DR N-PSDB; AAI65751.
XX
PT Identification of compounds modulating cellular receptor activity useful
PT for identifying and screening for ligands for orphan receptors, comprises
PT using recombinant cells comprising both receptors and test polypeptide.
XX
PS Example 5; Page 34; 50pp; English.
XX
CC The specification describes an assay for screening and identifying
CC pharmaceutically effective compounds that specifically interact with and
CC modulate the activity of a cellular receptor or ion channel. The assay
CC uses a mixture of recombinant cells, each comprising a receptor protein
CC whose signal transduction activity is modulated by an interaction with an
CC extracellular signal, a recombinant gene encoding a potential receptor

CC polypeptide, and a reporter gene construct. The assay is useful for rapid
CC screening of large numbers of polypeptides to identify polypeptides
CC antagonizing or agonizing receptor activity, and to identify drugs for
CC modulating cellular activity. It is especially useful to identify ligands
CC for orphan receptors, especially ligands for orphan cell surface
CC receptors, which are useful in drug discovery. The present sequence
CC represents an improved a-factor variant, which is a better substrate for
CC ABC transporters. The variant was identified using the assay of the
CC invention

XX

SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| | | |
Db 6 FFFLP 10

RESULT 24

AAB84510

ID AAB84510 standard; peptide; 11 AA.

XX

AC AAB84510;

XX

DT 05-SEP-2001 (first entry)

XX

DE Amino acid sequence of a pheromone analogue.

XX

KW G protein coupled receptor; GPCR; cellular receptor; ion channel;
KW surrogate ligand; orphan receptor; pheromone analogue.

XX

OS Synthetic.

XX

PN US6255059-B1.

XX

PD 03-JUL-2001.

XX

PF 17-JAN-1996; 96US-00582333.

XX

PR 31-MAR-1993; 93US-00041431.

PR 31-JAN-1994; 94US-00190328.

PR 20-SEP-1994; 94US-00309313.

PR 13-OCT-1994; 94US-00322137.

PR 05-JUN-1995; 95US-00463181.

XX

PA (CADU-) CADUS PHARM CORP.

XX

PI Klein CA, Murphy AJM, Fowlkes DM, Broach J, Manfredi J, Paul J;
PI Trueheart J;

XX

DR WPI; 2001-396979/42.

DR N-PSDB; AAH27821.

XX

PT Identifying a ligand for an orphan G protein coupled receptor comprises

PT using an recombinant yeast expression library.
XX
PS Example 5; Col 63; 128pp; English.
XX
CC The specification describes a method for identifying a ligand for an
CC orphan G protein coupled receptor (GPCR). The method comprises rapidly
CC screening large numbers of polypeptides in a yeast expression library to
CC identify those polypeptides which induce or antagonise receptor
CC bioactivity. The method is useful for screening and identifying
CC pharmaceutically effective compounds that specifically interact with and
CC modulate the activity of a cellular receptor or ion channel. The assay is
CC particularly amenable for identifying surrogate ligands for orphan
CC receptors. The present sequence represents a pheromone analogue,
CC identified using the method of the invention
XX
SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 25
ABU10264
ID ABU10264 standard; peptide; 11 AA.
XX
AC ABU10264;
XX
DT 28-JUL-2003 (first entry)
XX
DE Alpha-factor analogue peptide #3 from random peptide library.
XX
KW Engineered yeast cell; yeast pheromone system surrogate;
KW surrogate modulator; yeast pheromone system protein surrogate; trait;
KW antifungal compound; antibiotic; alpha-factor pheromone; MFalpha1.
XX
OS Synthetic.
XX
PN US2003008380-A1.
XX
PD 09-JAN-2003.
XX
PF 10-MAY-1999; 99US-00309196.
XX
PR 31-MAR-1993; 93US-00041431.
PR 31-JAN-1994; 94US-00190328.
PR 20-SEP-1994; 94US-00309313.
PR 13-OCT-1994; 94US-00322137.
XX
PA (FOWL/) FOWLKES D M.
PA (BROA/) BROACH J.
PA (MANF/) MANFREDI J.
PA (KLEI/) KLEIN C.

PA (MURP//) MURPHY A J.
PA (PAUL//) PAUL J.
PA (TRUE//) TRUEHEART J.
XX
PI Fowikes DM, Broach J, Manfredi J, Klein C, Murphy AJ, Paul J;
PI Trueheart J;
XX
DR WPI; 2003-416694/39.
DR N-PSDB; ACA61843.
XX
PT New yeast cell having a pheromone system, and which expresses a
PT heterologous surrogate of a yeast pheromone system, and a heterologous
PT peptide, useful in the discovery of antifungal compounds.
XX
PS Example 5; Page 35; 71pp; English.
XX
CC The present invention relates to engineered yeast cells expressing a
CC heterologous surrogate of a yeast pheromone system, and a heterologous
CC peptide that is a potential modulator of the surrogate. The surrogate
CC performs a function naturally performed by the corresponding yeast
CC pheromone system protein, under at least some conditions. Inhibition or
CC activation of the surrogate by the heterologous peptide affects a
CC selectable or screenable trait of the yeast cells. The yeast cells are
CC useful for producing pheromone system protein surrogates. They are also
CC useful in the discovery of antifungal compounds, in describing the use of
CC *Saccharomyces cerevisiae* mutant strains, which are made highly sensitive
CC to a large range of antibiotics, and for the rapid detection of
CC antifungals. The present sequence represents an alpha-factor analogue
CC peptide from a random peptide library
XX
SQ Sequence 11 AA;

Query Match 46.8%; Score 29; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
 |||||
Db 6 FFFLP 10

RESULT 26
AAB45712
ID AAB45712 standard; protein; 13 AA.
XX
AC AAB45712;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human 7TM clone HEOAD54 protein fragment #4.
XX
KW Transmembrane receptor protein; 7TM; gene therapy; human; bactericidal;
KW fungicidal; viricidal; anti-HIV; analgesic; cytostatic; anabolic;
KW anti-asthmatic; anti-parkinsonian; cardiant; hypotensive; hypertensive;
KW osteopathic; anti-ulcer; immunosuppressive; cerebroprotective; vaccine;
KW antidepressant; neuroprotective; heptahelical receptor; infection;
KW serpentine receptor; G-protein coupled receptor; cancer; anorexia;

KW bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; ulcer; myocardial infarction; allergy; benign prostatic hypertrophy; anxiety; schizophrenia; manic depression; Huntington's chorea.

XX

OS Homo sapiens.

XX

PN WO200071584-A1.

XX

PD 30-NOV-2000.

XX

PF 19-MAY-2000; 2000WO-US013737.

XX

PR 20-MAY-1999; 99US-0135167P.

PR 13-JUL-1999; 99US-0143616P.

PR 09-SEP-1999; 99US-0152934P.

PR 14-MAR-2000; 2000US-0189029P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Ni J, Soppet DR, Li Y, Fan P;

XX

DR WPI; 2001-025139/03.

DR N-PSDB; AAC82668.

XX

PT Nucleic acids encoding human 7 transmembrane receptor polypeptides, useful for preventing, diagnosing and treating e.g. asthma, Parkinson's disease and ulcers.

XX

PS Claim 1b; Page 281; 288pp; English.

XX

CC This invention describes novel nucleic acid molecules (I) encoding human 7 transmembrane (7TM) receptor polypeptides (also called heptahelical, serpentine or G-protein coupled receptors). The products of the invention have bactericidal, fungicidal, viricidal, anti-HIV, analgesic, cytostatic, anabolic, anti-asthmatic, anti-parkinsonian, cardiant, hypotensive, hypertensive, osteopathic, anti-ulcer, immunosuppressive, cerebroprotective, antidepressant and neuroprotective activity and can be used in gene therapy or in a vaccine. (I) and the 7TM receptor protein it encodes may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate 7TM receptor expression. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence which patients may be in need of restorative therapy. Diseases associated with inappropriate 7TM receptor polypeptide expression include for example bacterial, fungal and viral (especially human immuno-deficiency virus) infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertrophy, anxiety, schizophrenia, manic depression and Huntington's chorea

XX

SQ Sequence 13 AA;

Query Match 46.8%; Score 29; DB 4; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;

Matches	6;	Conservative	2;	Mismatches	3;	Indels	0;	Gaps	0;
QY	1	LFFF LPV VNV L	11						
		:	:						
Db	2	LEFF LPL ALIL	12						

RESULT 27

ABG67849

ID ABG67849 standard; peptide; 14 AA.

XX

AC ABG67849;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human ADPI tryptic digest peptide #558.

XX

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
KW Alzheimer's disease-associated feature; neuroprotective;
KW Alzheimer's disease-associated protein isoform; nootropic;
KW ADPI tryptic digest peptide.

XX

OS Homo sapiens.

XX

PN WO200246767-A2.

XX

PD 13-JUN-2002.

XX

PF 29-NOV-2001; 2001WO-GB005289.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAC, Parekh RB, Rohlf C;

XX

DR WPI; 2002-508575/54.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.

XX

PS Claim 7; Page 53; 427pp; English.

XX

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the
CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy

CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides

XX

SQ Sequence 14 AA;

Query Match 46.8%; Score 29; DB 5; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNVL P 12
| :|||||
Db 4 PPINVLP 10

RESULT 28

ADA24208

ID ADA24208 standard; peptide; 14 AA.

XX

AC ADA24208;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alzheimer's disease-associated protein isoform tryptic peptide #813.

XX

KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.

XX

OS Homo sapiens.

XX

PN US2003064411-A1.

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00014340.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

PA (ROHL/) ROHLFF C.

XX

PI Herath HMAC, Parekh RB, Rohlff C;

XX

DR WPI; 2003-540784/51.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 813; 115pp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 14 AA;

Query Match 46.8%; Score 29; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
| :|||||
Db 4 PPINVLP 10

RESULT 29
ADA23994
ID ADA23994 standard; peptide; 14 AA.
XX
AC ADA23994;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #603.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.
XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2003-540784/51.

XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 603; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 14 AA;

Query Match 46.8%; Score 29; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 6 PVVNVL 12
| :|||||
Db 4 PPINVLP 10

RESULT 30
ADA23993
ID ADA23993 standard; peptide; 14 AA.
XX
AC ADA23993;
XX
DT 20-NOV-2003 (first entry)
XX
DE Alzheimer's disease-associated protein isoform tryptic peptide #602.
XX
KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
KW Alzheimer's disease-associated protein isoform; ADPI.
XX
OS Homo sapiens.
XX
PN US2003064411-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00014340.
XX
PR 08-DEC-2000; 2000US-0254431P.

XX
PA (HERA/) HERATH H M A C.
PA (PARE/) PAREKH R B.
PA (ROHL/) ROHLFF C.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2003-540784/51.
XX
PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 602; 115pp; English.
XX
CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.
XX
SQ Sequence 14 AA;

Query Match 46.8%; Score 29; DB 6; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 6 PVVNVL P 12
| :|||||
Db 4 PPINVLP 10

RESULT 31
AAB89134
ID AAB89134 standard; peptide; 18 AA.
XX
AC AAB89134;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #227.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX

PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Example 3; Page 43; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 46.8%; Score 29; DB 4; Length 18;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFPLPVVNVL 11
| |||:: ::
Db 6 LGFFLPLLTMI 16

RESULT 32
AAB89135
ID AAB89135 standard; peptide; 18 AA.
XX
AC AAB89135;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #228.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.

XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Example 3; Page 43; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 46.8%; Score 29; DB 4; Length 18;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFLPVVNVL 11
| |||:: ::
Db 2 LGFFLPLLTMI 12

RESULT 33
ABJ37110
ID ABJ37110 standard; peptide; 18 AA.
XX
AC ABJ37110;
XX
DT 08-MAY-2003 (first entry)
XX
DE Concatameric immunoadhesion CTLA-4 leader peptide #1.
XX
KW Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
KW antiarthritic; immunomodulator; concatameric protein; soluble domain;
KW dimeric protein; inflammation; septicaemia; cytotoxicity;
KW rheumatoid arthritis; cachexia; inflammation.
XX
OS Unidentified.
XX
PN WO2003010202-A1.
XX
PD 06-FEB-2003.
XX
PF 26-JUL-2002; 2002WO-KR001427.
XX
PR 26-JUL-2001; 2001KR-00045028.
XX

PA (MEDE-) MEDEXGEN CO LTD.
XX
PI Chung Y, Han J, Lee H, Choi E, Kim J;
XX
DR WPI; 2003-229639/22.
XX
PT New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.
XX
PS Claim 24; Page 70; 211pp; English.
XX
CC The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical
CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicaemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents a CTLA-4 leader peptide
CC relating to the human concatameric protein of the invention
XX
SQ Sequence 18 AA;

Query Match 46.8%; Score 29; DB 6; Length 18;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFF LPV 7
| ||:||
Db 8 LLFF I PV 14

RESULT 34
AAW81861
ID AAW81861 standard; peptide; 8 AA.
XX
AC AAW81861;
XX
DT 05-FEB-1999 (first entry)
XX
DE Human proinsulin analogue HB101 peptide 4.
XX
KW Proinsulin; yield increase; secretion; connecting peptide; A chain;
KW B chain.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5840542-A.
XX
PD 24-NOV-1998.
XX
PF 28-JUL-1995; 95US-00508664.
XX

PR 28-JUL-1995; 95US-00508664.
XX
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
PI Yoon J, Kang Y;
XX
DR WPI; 1999-034039/03.
XX
PT Increasing secreted yields of recombinant proinsulin - by expressing
PT proinsulin with deletions in connecting peptide region.
XX
PS Example 6; Col 7-8; 13pp; English.
XX
CC This peptide is used in the construction of novel human derived ZZ-
CC proinsulin analogues which are used in a method to increase the yield of
CC proinsulin secreted by bacterial cells transformed with a proinsulin
CC expression vector. This method involves modifying the vector so that the
CC connecting peptide region of the encoded proinsulin (linking the A and B
CC chains) is deleted or comprises the amino acid RREAEDQGSLQKR,
CC RREAEDLQVGQVE or RRE
XX
SQ Sequence 8 AA;

Query Match 45.2%; Score 28; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
||: |||
Db 1 FFYTPIV 7

RESULT 35
ABP75281
ID ABP75281 standard; peptide; 9 AA.
XX
AC ABP75281;
XX
DT 20-FEB-2003 (first entry)
XX
DE Chlamydia pneumonia peptide epitope #47.
XX
KW Antibacterial; secreted protein; intracellular bacterium.
XX
OS Chlamydia pneumonia.
XX
PN WO200282091-A2.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002WO-DK000234.
XX
PR 09-APR-2001; 2001DK-00000581.
PR 09-APR-2001; 2001US-0282513P.
XX
PA (SHAW/) SHAW A C.
PA (VAND/) VANDAHL B B.

XX
PI Shaw AC, Vandahl BB;
XX
DR WPI; 2003-058585/05.
XX
PT Identifying intracellular bacterial proteins by labeling proteins in the
PT presence of a eukaryotic protein synthesis inhibitor, performing
PT electrophoresis, autoradiography and comparing profiles to an infected-
PT cell lysate profile.
XX
PS Claim 34; Page 146; 179pp; English.
XX
CC The present invention relates to a method (M1) for identifying secreted
CC intracellular bacterial proteins (BP). M1 comprises: (a) selectively
CC visualising BP by pulse labelling in the presence of an inhibitor of
CC eukaryotic protein synthesis followed by 2D electrophoresis and
CC autoradiography; (b) comparing protein profiles (PF) of purified bacteria
CC to PF of total lysate (TL) of infected cells; and (c) identifying protein
CC spots present in differential images from gels loaded with TL. The
CC present sequence is one such bacterial peptide epitope which was
CC identified by the method of the invention
XX
SQ Sequence 9 AA;

Query Match 45.2%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNVL 11
|||:|||
Db 1 FLPIILV 8

RESULT 36
ABP75273
ID ABP75273 standard; peptide; 9 AA.
XX
AC ABP75273;
XX
DT 20-FEB-2003 (first entry)
XX
DE Chlamydia pneumonia peptide epitope #39.
XX
KW Antibacterial; secreted protein; intracellular bacterium.
XX
OS Chlamydia pneumonia.
XX
PN WO200282091-A2.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002WO-DK000234.
XX
PR 09-APR-2001; 2001DK-00000581.
PR 09-APR-2001; 2001US-0282513P.
XX
PA (SHAW/) SHAW A C.

PA (VAND/) VANDAHL B B.
XX
PI Shaw AC, Vandahl BB;
XX
DR WPI; 2003-058585/05.
XX
PT Identifying intracellular bacterial proteins by labeling proteins in the
PT presence of a eukaryotic protein synthesis inhibitor, performing
PT electrophoresis, autoradiography and comparing profiles to an infected-
PT cell lysate profile.
XX
PS Claim 34; Page 143; 179pp; English.
XX
CC The present invention relates to a method (M1) for identifying secreted
CC intracellular bacterial proteins (BP). M1 comprises: (a) selectively
CC visualising BP by pulse labelling in the presence of an inhibitor of
CC eukaryotic protein synthesis followed by 2D electrophoresis and
CC autoradiography; (b) comparing protein profiles (PF) of purified bacteria
CC to PF of total lysate (TL) of infected cells; and (c) identifying protein
CC spots present in differential images from gels loaded with TL. The
CC present sequence is one such bacterial peptide epitope which was
CC identified by the method of the invention
XX
SQ Sequence 9 AA;

Query Match 45.2%; Score 28; DB 6; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.4e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVVNV 10
| |||:: |
Db 1 FTFLPIILV 9

RESULT 37
AAG64341
ID AAG64341 standard; peptide; 15 AA.
XX
AC AAG64341;
XX
DT 24-SEP-2001 (first entry)
XX
DE Ribosomal protein L2-11 peptide fragment.
XX
KW Ribosomal protein L2-11; cytostatic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation.
XX
OS Unidentified.
XX
PN WO200147990-A1.
XX
PD 05-JUL-2001.
XX
PF 18-DEC-2000; 2000WO-CN000630.
XX
PR 24-DEC-1999; 99CN-00125768.

XX
PA (BIOW-) BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-425641/45.
XX
PT Ribosomal protein L2-11 and encoded polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation.
XX
PS Example 6; Page 14; 35pp; Chinese.
XX
CC The present invention relates to ribosomal protein L2-11 and its coding
CC sequence (see AAH49665 and AAG64340). The ribosomal protein and its
CC coding sequence are useful in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is a N-terminal peptide fragment of
CC the ribosomal protein, which was used in an example from the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 45.2%; Score 28; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVVNVL 11
||||| :::
Db 4 FFLPVGSMI 12

RESULT 38
AAB23686
ID AAB23686 standard; peptide; 9 AA.
XX
AC AAB23686;
XX
DT 05-JAN-2001 (first entry)
XX
DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:38.
XX
KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytostatic; immunostimulant; cellular immune response inducer;
KW protozoacide; leukaemia; cancer.
XX
OS Homo sapiens.
XX
PN WO200049041-A1.
XX
PD 24-AUG-2000.
XX
PF 18-FEB-2000; 2000WO-JP000941.
XX
PR 19-FEB-1999; 99JP-00041535.
XX

PA (SUME) SUMITOMO ELECTRIC IND CO.

XX

PI Shinbara N, Udono H, Yui K;

XX

DR WPI; 2000-543748/49.

XX

PT Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer.

XX

PS Claim 7; Page 60; 72pp; Japanese.

XX

CC The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed CTL epitope for use in a fused protein of the present invention

XX

SQ Sequence 9 AA;

Query Match 43.5%; Score 27; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LP 6

::::|

Db 1 VYFF LP 6

RESULT 39

ABG79052

ID ABG79052 standard; peptide; 9 AA.

XX

AC ABG79052;

XX

DT 15-NOV-2002 (first entry)

XX

DE Human Gp100 class I HLA restricted melanocyte antigen peptide #15.

XX

KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen; lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA; cytostatic; human.

XX

OS Homo sapiens.

XX

PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.

XX
PS Disclosure; Page 16; 61pp; English.

XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention

XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 27; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LP 6
:::|||||
Db 1 VYFF LP 6

RESULT 40
AAO17100

ID AAO17100 standard; peptide; 9 AA.
XX
AC AAO17100;
XX
DT 06-JUN-2002 (first entry)
XX
DE Human gp100 protein antigen SEQ ID NO: 20.
XX
KW Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
KW virucide; cancer; hepatitis B virus.
XX
OS Homo sapiens.
XX
PN WO200216560-A1.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-EP009790.
XX
PR 24-AUG-2000; 2000DE-01041515.
XX
PA (SCHU/) SCHULER G.
XX
PI Schuler G, Schuler-Thurner B;
XX
DR WPI; 2002-292062/33.
XX
PT Preparation of cryopreserved, mature dendritic cells, useful in vaccines,
PT comprises culturing immature cells on medium containing cocktail of
PT maturation factors, then freezing.
XX
PS Disclosure; Fig 28; 87pp; German.
XX
CC The present invention relates to a method for the preparation of ready-
CC for-use, cryopreserved, mature dendritic cells comprising growing
CC immature dendritic cells in a culture medium that includes a 'maturation
CC cocktail' of one or more maturation stimuli and freezing the resulting
CC matured cells in a freezing medium that does not contain heterologous
CC serum. When loaded with antigens, the dendritic cells can be used as
CC vaccines, e.g. against tumours and hepatitis B virus. The present
CC sequence is an antigen described in the invention
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 27; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LFFFPLP 6
Db 1 VYFFLP 6

RESULT 41
ABG66788
ID ABG66788 standard; peptide; 9 AA.
XX

AC ABG66788;
XX
DT 24-SEP-2002 (first entry)
XX
DE Tumour antigen Gp100, HLA-A2 epitope #8.
XX
KW Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;
KW human leukocyte antigen; fusion protein; epitope; cytostatic; tumour;
KW gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer;
KW liver cancer; biliary tract cancer; pancreatic cancer; vaccine;
KW prostatic cancer; testicular cancer; lung cancer; breast cancer;
KW malignant melanoma; mesothelioma; brain tumour; ovarian cancer;
KW uterine cancer; cervical cancer; head and neck cancer; bladder cancer;
KW Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma;
KW acquired immunodeficiency syndrome; AIDS-related lymphoma.
XX
OS Homo sapiens.
XX
PN WO200236146-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-GB004844.
XX
PR 02-NOV-2000; 2000GB-00026812.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G, Hunter M;
XX
DR WPI; 2002-508108/54.
XX
PT New polynucleotide capable of expressing an epitope-beta2m fusion protein
PT useful for generating cytotoxic T lymphocyte responses against a tumor
PT and in restoring antigen presentation in the tumor of a host.
XX
PS Disclosure; Page 24; 46pp; English.
XX
CC The invention relates to a new polynucleotide capable of expressing an
CC epitope-beta_2m fusion protein useful for generating cytotoxic T
CC lymphocyte (CTL) responses against a tumour or in restoring antigen
CC presentation in the tumour of a host. Also included are a polynucleotide
CC capable of expressing an epitope-beta_2m fusion protein in combination
CC with a vaccination agent that stimulates a CTL response against the
CC epitope of the fusion protein for simultaneous, separate or sequential
CC use in the treatment of cancer and a method of treating a tumour by
CC administering a capable of expressing an epitope-beta_2m fusion protein,
CC and optionally a vaccination agent that stimulates a CTL response against
CC the epitope of the fusion protein. The polynucleotide is useful for
CC generating CTL responses against tumours, for restoring antigen
CC presentation in the tumour, and subsequently for treating cancers, such
CC as gastrointestinal tumour, prostatic, testicular, lung or breast cancer,
CC malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine
CC cancer including cervical cancer, cancer of the head and neck, bladder
CC cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome)-
CC related Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and
CC haematopoietic malignant tumours such as leukaemia and lymphoma. The

CC epitope is an HLA (human leukocyte antigen) peptide derived from a viral
CC or tumour antigen. The present sequence is a tumour HLA epitope used in
CC the fusion proteins of the invention

XX

SQ Sequence 9 AA;

Query Match 43.5%; Score 27; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFPLP 6
::|||
Db 1 VYFFPLP 6

RESULT 42

ABJ19645

ID ABJ19645 standard; peptide; 10 AA.

XX

AC ABJ19645;

XX

DT 03-APR-2003 (first entry)

XX

DE Neuronal nitric oxide synthase related peptide fragment SEQ ID No 103.

XX

KW Antidiabetic; neuronal nitric oxide synthase; nNOS; enzyme; PIN;
KW inhibitor; insulin response; prediabetic; hyperinsulinic;
KW type 2 diabetes; rat.

XX

OS Synthetic.

XX

PN WO200283936-A2.

XX

PD 24-OCT-2002.

XX

PF 17-APR-2002; 2002WO-FR001327.

XX

PR 18-APR-2001; 2001FR-00005248.

XX

PA (INNO-) INNODIA.

XX

PI Gross R, Lajoix A, Ribes G;

XX

DR WPI; 2003-111816/10.

XX

PT Identifying compounds that modulate interaction of neuronal nitric oxide
PT synthase and its inhibitor, useful e.g. for treating prediabetic states.

XX

PS Claim 10; Page 44; 89pp; French.

XX

CC The invention relates to a novel method for detecting compounds that
CC modulate the complexation between neuronal nitric oxide synthase (nNOS)
CC and the inhibitor of nNOS (PIN). The nNOS protein comprises a 1429 amino
CC acid sequence, fully defined in the specification, or its variants. The
CC nNOS protein, its peptide fragments identified by the new method, and the
CC compound 1-(4-ethoxyphenyl)-5-(5-(benzimidazol-2-ylthio)-fur-2-
CC ylmethylidene)-hexahydropyrimidin-2,4,6-trione are used to treat altered

CC insulin responses in prediabetic and hyperinsulinic states, and in
CC subjects with type 2 diabetes. This sequence represents an nNOS peptide
CC fragment relating to the invention

XX

SQ Sequence 10 AA;

Query Match 43.5%; Score 27; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
||:|||
Db 4 PVLSILP 10

RESULT 43

AAV93625

ID AAV93625 standard; peptide; 11 AA.

XX

AC AAV93625;

XX

DT 25-SEP-2000 (first entry)

XX

DE Peptide agonist for formyl peptide receptor like-1 receptor.

XX

KW Surrogate ligand; formyl peptide receptor like-1 receptor;
KW FPRL-1 receptor; signal transduction; cellular receptor; ion channel.

XX

OS Synthetic.

XX

PN WO200031261-A2.

XX

PD 02-JUN-2000.

XX

PF 24-NOV-1999; 99WO-US027909.

XX

PR 25-NOV-1998; 98US-0109902P.

PR 30-NOV-1998; 98US-00201396.

XX

PA (CADU-) CADUS PHARM CORP.

XX

PI Klein CA, Murphy AJ, Paul J;

XX

DR WPI; 2000-400071/34.

XX

PT Recombinant cell used to identify modulators of heterologous formyl
PT peptide receptor like-1 (FPRL-1) receptor, comprising FPRL-1 receptor
PT expressed in the cell membrane, and a FPRL-1 receptor ligand agonist.

XX

PS Claim 17; Page 66; 156pp; English.

XX

CC The present sequence represents a peptide agonist for a heterologous
CC formyl peptide receptor like-1 (FPRL-1) receptor. The specification
CC describes a cell which expresses FPRL-1 in the cell membrane, so that
CC extracellular signal interaction with the receptors extracellular region
CC modulates signal transduction via the receptor. The cell is used in a
CC method to screen and identify pharmaceutically effective compounds which

CC specifically interact with and modulate the activity of a cellular
CC receptor or ion channel, especially the FPRL-1 receptor

XX

SQ Sequence 11 AA;

Query Match 43.5%; Score 27; DB 3; Length 11;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
||| ||
Db 3 FFFRPV 8

RESULT 44

AAU09823

ID AAU09823 standard; peptide; 14 AA.

XX

AC AAU09823;

XX

DT 14-FEB-2002 (first entry)

XX

DE Modified ovalbumin-derived class I H-2Kb restricted peptide #3.

XX

KW Ovalbumin-derived class I H-2Kb restricted peptide; vaccine;
KW immunostimulant; immunogenic; interferon-gamma-producing T cell; IFN;
KW popliteal lymph node; spleen; immune response; systemic response.

XX

OS Synthetic.

XX

PN WO200178767-A2.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-EP004313.

XX

PR 14-APR-2000; 2000AT-00000657.

XX

PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

XX

PI Mattner F, Zauner W, Schmidt W, Buschle M;

XX

DR WPI; 2002-025970/03.

XX

PT Pharmaceutical preparation for use as a potent vaccine for inducing an
PT improved immune response in a mammal, comprises a modified peptide.

XX

PS Example 1; Page 9; 18pp; English.

XX

CC The invention relates to a pharmaceutical preparation comprising a
CC modified peptide, which induces an improved immune response in a mammal
CC compared to the wild type peptide. The neutral peptide (SIINFEKL) (one
CC negatively charged (Glu), one positively charged (Lys) amino acid) was
CC rendered negative by adding (at the N-terminus) Glu Glu or Glu Asp Glu
CC Asp, respectively. Results showed that the addition of 4 negatively-
CC charged amino acids (EDED) at the N-terminus of peptide SIINFEKL makes
CC this peptide (in combination with poly-L-arginine) able to induce a high

CC amount of specific interferon (IFN)-gamma-producing T cells in the
CC draining (popliteal) lymph node (local response) and in the spleen
CC (systemic response). Thus, the addition of hydrophobic amino acids as
CC well as the addition of negatively charged amino acids transforms the
CC peptide SIINFEKL to a good inducer of specific T cells. The modified
CC peptides of the pharmaceutical composition induce a stronger immune
CC response in a mammal compared to wild type antigens. The present sequence
CC represents modified ovalbumin-derived class I H-2K^b restricted peptide #3
CC as described in the method of the invention

XX

SQ Sequence 14 AA;

Query Match 43.5%; Score 27; DB 5; Length 14;
Best Local Similarity 33.3%; Pred. No. 5.5e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LFFFPLPVVN 9
:| |: ::|
Db 2 IFIFISIIN 10

RESULT 45

AAY98981

ID AAY98981 standard; peptide; 15 AA.

XX

AC AAY98981;

XX

DT 07-AUG-2000 (first entry)

XX

DE HLA class II binding antigen epitope peptide #170.

XX

KW Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
KW immune response; chronic viral disease; cancer; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
KW glomerulonephritis; food hypersensitivity; malaria.

XX

OS Unidentified.

XX

PN WO9961916-A1.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US012066.

XX

PR 29-MAY-1998; 98US-0087192P.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Southwood S, Sidney J;

XX

DR WPI; 2000-097143/08.

XX

PT New compositions containing immunogenic peptide epitopes for various HLA
PT class II DR molecules useful for inducing helper T cell response.

XX

PS Claim 1; Page 42; 60pp; English.

XX

CC The present invention relates to a new pharmaceutical composition
CC comprising a unit dose form of a peptide, or analogue, comprising an
CC epitope selected from those represented by peptides AAY98812-Y99339 which
CC are derived from various antigens for various human leucocyte antigen
CC class DR molecules, representative of the world wide population. The
CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
CC helper T cell response. The pharmaceutical focuses the immune response
CC towards selected determinants and could therefore be used in cases of
CC chronic viral diseases and cancer. Examples of diseases that can be
CC treated using the peptide containing pharmaceutical include autoimmune
CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-
CC streptococcal endocarditis or glomerulonephritis and food
CC hypersensitivities. The peptide epitopes can be used to enhance immune
CC responses against other immunogens administered with the peptides.
CC Diseases which can be treated using immunogenic mixtures include prostate
CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
CC used to make monoclonal antibodies useful as potential diagnostic or
CC therapeutic agents. The peptides may also be useful as diagnostic
CC reagents, for example, to determine the susceptibility of an individual
CC to a treatment regimen. Also, the peptides may be used to predict which
CC individuals will be at substantial risk of developing chronic infection.
CC The selection of appropriate T and B cell epitopes should allow the
CC development of epitope based vaccines particularly towards conserved
CC epitopes of pathogens which are characterized by high sequence
CC variability such as HIV, HCV and Malaria

XX

SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 3; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy

1 LFFFPLPVVNVL 12
| | : || | : |

Db

2 LVFGIEVVEVVP 13

RESULT 46

AAG84564

ID AAG84564 standard; peptide; 15 AA.

XX

AC AAG84564;

XX

DT 10-SEP-2001 (first entry)

XX

DE MAGE2 DR supermotif binding peptide #29.

XX

KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.

XX

OS Homo sapiens.

OS Synthetic.

XX
PN WO200142267-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033545.
XX
PR 10-DEC-1999; 99US-00458298.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-375002/39.
XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
PS Disclosure; Page 134; 171pp; English.
XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVVNVL 12
| | : || |:
Db 3 LVFGIEVVEVVP 14

RESULT 47
AAG84573
ID AAG84573 standard; peptide; 15 AA.
XX
AC AAG84573;

XX
DT 10-SEP-2001 (first entry)
XX
DE MAGE2 DR supermotif binding peptide #38.
XX
KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142267-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033545.
XX
PR 10-DEC-1999; 99US-00458298.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-375002/39.
XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
PS Disclosure; Page 134; 171pp; English.
XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVNVLP 12
| | : || |:
Db 2 LVFGIEVVEVVP 13

RESULT 48

AAG84885

ID AAG84885 standard; peptide; 15 AA.

XX

AC AAG84885;

XX

DT 10-SEP-2001 (first entry)

XX

DE MAGE2 DR3 binding peptide #4.

XX

KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200142267-A1.

XX

PD 14-JUN-2001.

XX

PF 11-DEC-2000; 2000WO-US033545.

XX

PR 10-DEC-1999; 99US-00458298.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

XX

DR WPI; 2001-375002/39.

XX

PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.

XX

PS Example 5; Page 164; 171pp; English.

XX

CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the

CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention

XX

SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LFFFPLPVVNVL P 12
| | : || |:
Db 2 LVFGIEVVEVVP 13

RESULT 49

AAG84649

ID AAG84649 standard; peptide; 15 AA.

XX

AC AAG84649;

XX

DT 10-SEP-2001 (first entry)

XX

DE MAGE2 DR 3a motif binding peptide #8.

XX

KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200142267-A1.

XX

PD 14-JUN-2001.

XX

PF 11-DEC-2000; 2000WO-US033545.

XX

PR 10-DEC-1999; 99US-00458298.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;

XX

DR WPI; 2001-375002/39.

XX

PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.

XX

PS Disclosure; Page 142; 171pp; English.

XX

CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second

CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention

XX

SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFF LPV VNVL P 12
| | : || | : |
Db 2 LVFG GIEV VEV VP 13

RESULT 50

AAY21126

ID AAY21126 standard; protein; 17 AA.

XX

AC AAY21126;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human bcl2 proto-oncogene wild type protein fragment 23.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

XX

PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX

DR WPI; 1998-609901/51.

DR N-PSDB; AAX75766.

XX

PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and

PT neurological diseases, particularly Alzheimer's disease, and also for

PT treatment and prevention with specific ribozymes or wild-type RNA.

XX

PS Disclosure; Fig 15; 258pp; English.

XX

CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC use of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A

XX

SQ Sequence 17 AA;

Query Match 43.5%; Score 27; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8

|| ||:|

Db 6 FFKLPIV 12

Search completed: July 4, 2004, 04:40:43

Job time : 32.1194 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 7.52239 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-4

Perfect score: 62

Sequence: 1 LFFFPLPVVNVL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	62	100.0	12	4	US-09-641-803-4	Sequence 4, Appli
2	29	46.8	11	1	US-08-464-531-57	Sequence 57, Appl
3	29	46.8	11	2	US-08-461-598-57	Sequence 57, Appl
4	29	46.8	11	3	US-08-322-137-57	Sequence 57, Appl
5	29	46.8	11	3	US-08-582-333A-68	Sequence 68, Appl
6	28	45.2	8	2	US-08-508-664-20	Sequence 20, Appl
7	27	43.5	18	6	5185441-4	Patent No. 5185441
8	26	41.9	10	3	US-09-328-501-7	Sequence 7, Appli
9	26	41.9	10	4	US-09-777-710A-7	Sequence 7, Appli
10	26	41.9	16	4	US-09-009-953-15	Sequence 15, Appl
11	25	40.3	10	3	US-08-159-339A-1023	Sequence 1023, Ap

12	25	40.3	13	2	US-08-194-981E-16	Sequence 16, Appl
13	25	40.3	17	3	US-09-177-249-88	Sequence 88, Appl
14	25	40.3	18	3	US-08-482-918-94	Sequence 94, Appl
15	25	40.3	18	3	US-08-482-918-95	Sequence 95, Appl
16	25	40.3	18	3	US-09-224-681-94	Sequence 94, Appl
17	25	40.3	18	3	US-09-224-681-95	Sequence 95, Appl
18	25	40.3	18	3	US-08-336-728A-94	Sequence 94, Appl
19	25	40.3	18	3	US-08-336-728A-95	Sequence 95, Appl
20	24	38.7	7	3	US-09-103-478-5	Sequence 5, Appli
21	24	38.7	7	3	US-09-103-478-17	Sequence 17, Appl
22	24	38.7	7	4	US-09-193-931C-5	Sequence 5, Appli
23	24	38.7	7	4	US-09-193-931C-17	Sequence 17, Appl
24	24	38.7	7	4	US-09-026-221-5	Sequence 5, Appli
25	24	38.7	7	4	US-09-026-221-17	Sequence 17, Appl
26	24	38.7	9	2	US-08-934-222-106	Sequence 106, App
27	24	38.7	9	2	US-08-933-402-106	Sequence 106, App
28	24	38.7	9	2	US-09-207-621-106	Sequence 106, App
29	24	38.7	9	2	US-08-532-818-106	Sequence 106, App
30	24	38.7	9	3	US-09-231-797-106	Sequence 106, App
31	24	38.7	9	3	US-08-934-224-106	Sequence 106, App
32	24	38.7	9	3	US-08-933-843-106	Sequence 106, App
33	24	38.7	9	3	US-08-934-223-106	Sequence 106, App
34	24	38.7	9	3	US-09-413-492-106	Sequence 106, App
35	24	38.7	12	4	US-10-118-575A-7	Sequence 7, Appli
36	24	38.7	13	5	PCT-US94-10257A-16	Sequence 16, Appl
37	24	38.7	16	4	US-08-213-419B-7	Sequence 7, Appli
38	23	37.1	7	2	US-08-559-492-10	Sequence 10, Appl
39	23	37.1	8	4	US-09-171-337A-17	Sequence 17, Appl
40	23	37.1	8	4	US-09-631-022-17	Sequence 17, Appl
41	23	37.1	8	4	US-08-979-847B-150	Sequence 150, App
42	23	37.1	8	4	US-08-979-847B-151	Sequence 151, App
43	23	37.1	8	4	US-08-979-847B-152	Sequence 152, App
44	23	37.1	9	3	US-08-159-339A-1217	Sequence 1217, Ap
45	23	37.1	9	3	US-08-159-339A-1218	Sequence 1218, Ap
46	23	37.1	9	4	US-09-492-543-149	Sequence 149, App
47	23	37.1	9	4	US-09-492-543-159	Sequence 159, App
48	23	37.1	9	4	US-09-527-487-5	Sequence 5, Appli
49	23	37.1	10	3	US-08-159-339A-1219	Sequence 1219, Ap
50	23	37.1	11	2	US-08-508-664-13	Sequence 13, Appl
51	23	37.1	14	3	US-09-082-420-16	Sequence 16, Appl
52	23	37.1	15	3	US-08-159-339A-1215	Sequence 1215, Ap
53	23	37.1	15	4	US-09-009-953-176	Sequence 176, App
54	23	37.1	15	4	US-09-148-545-224	Sequence 224, App
55	23	37.1	15	4	US-09-947-372A-28	Sequence 28, Appl
56	23	37.1	15	5	PCT-US93-06751-86	Sequence 86, Appl
57	23	37.1	16	4	US-09-009-953-25	Sequence 25, Appl
58	23	37.1	17	4	US-09-148-545-221	Sequence 221, App
59	23	37.1	18	1	US-08-451-472-18	Sequence 18, Appl
60	23	37.1	18	1	US-08-451-472-48	Sequence 48, Appl
61	23	37.1	18	1	US-08-451-472-68	Sequence 68, Appl
62	23	37.1	18	4	US-09-171-337A-16	Sequence 16, Appl
63	23	37.1	18	4	US-09-631-022-16	Sequence 16, Appl
64	22.5	36.3	9	4	US-09-311-784A-454	Sequence 454, App
65	22.5	36.3	15	4	US-09-009-953-51	Sequence 51, Appl
66	22.5	36.3	15	4	US-09-009-953-54	Sequence 54, Appl
67	22.5	36.3	15	4	US-09-009-953-60	Sequence 60, Appl
68	22.5	36.3	15	4	US-09-009-953-63	Sequence 63, Appl

69	22	35.5	8	3	US-08-444-818-475	Sequence 475, App
70	22	35.5	9	2	US-08-934-222-43	Sequence 43, Appl
71	22	35.5	9	2	US-08-933-402-43	Sequence 43, Appl
72	22	35.5	9	2	US-09-207-621-43	Sequence 43, Appl
73	22	35.5	9	2	US-08-532-818-43	Sequence 43, Appl
74	22	35.5	9	2	US-08-942-819-9	Sequence 9, Appli
75	22	35.5	9	3	US-08-159-339A-652	Sequence 652, App
76	22	35.5	9	3	US-08-159-339A-694	Sequence 694, App
77	22	35.5	9	3	US-08-159-339A-695	Sequence 695, App
78	22	35.5	9	3	US-09-231-797-43	Sequence 43, Appl
79	22	35.5	9	3	US-08-934-224-43	Sequence 43, Appl
80	22	35.5	9	3	US-08-933-843-43	Sequence 43, Appl
81	22	35.5	9	3	US-08-934-223-43	Sequence 43, Appl
82	22	35.5	9	3	US-09-413-492-43	Sequence 43, Appl
83	22	35.5	9	4	US-09-492-543-59	Sequence 59, Appl
84	22	35.5	9	4	US-09-492-543-92	Sequence 92, Appl
85	22	35.5	9	4	US-09-492-543-129	Sequence 129, App
86	22	35.5	9	4	US-09-522-955A-9	Sequence 9, Appli
87	22	35.5	10	3	US-08-159-339A-717	Sequence 717, App
88	22	35.5	10	3	US-08-159-339A-718	Sequence 718, App
89	22	35.5	10	3	US-08-159-339A-719	Sequence 719, App
90	22	35.5	11	1	US-08-552-907-16	Sequence 16, Appl
91	22	35.5	11	2	US-08-486-839-10	Sequence 10, Appl
92	22	35.5	11	3	US-08-691-045-16	Sequence 16, Appl
93	22	35.5	11	3	US-09-151-011-10	Sequence 10, Appl
94	22	35.5	11	4	US-09-343-623-10	Sequence 10, Appl
95	22	35.5	11	6	5250516-6	Patent No. 5250516
96	22	35.5	12	1	US-08-290-301-67	Sequence 67, Appl
97	22	35.5	12	3	US-09-035-749-6	Sequence 6, Appli
98	22	35.5	12	3	US-09-003-903-12	Sequence 12, Appl
99	22	35.5	12	4	US-09-013-598-67	Sequence 67, Appl
100	22	35.5	12	4	US-08-811-519-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-641-803-4

; Sequence 4, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-4

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF LPV VNV LP 12
| | | | | | | | | | | |
Db 1 LFFF LPV VNV LP 12

RESULT 2

US-08-464-531-57

; Sequence 57, Application US/08464531
; Patent No. 5789184

; GENERAL INFORMATION:

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua

; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE

; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,531
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/041,431

;
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWES=2G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-531-57

Query Match 46.8%; Score 29; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 3
US-08-461-598-57
; Sequence 57, Application US/08461598
; Patent No. 5876951
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,598
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLKES=2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-598-57

Query Match 46.8%; Score 29; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFLP 6
| || || |
Db 6 FFFLP 10

RESULT 4
US-08-322-137-57
; Sequence 57, Application US/08322137
; Patent No. 6100042
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.

;
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,137
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWES=2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-322-137-57

Query Match 46.8%; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| || || |
Db 6 FFFLP 10

RESULT 5

US-08-582-333A-68

; Sequence 68, Application US/08582333A
; Patent No. 6255059
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD

;
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,333A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine J. Kara
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-582-333A-68

Query Match 46.8%; Score 29; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 6

US-08-508-664-20

; Sequence 20, Application US/08508664
; Patent No. 5840542
; GENERAL INFORMATION:
; APPLICANT: KANG, Yup
; APPLICANT: YOON, Ji-Won
; TITLE OF INVENTION: METHOD FOR MANUFACTURE OF PROINSULIN
; TITLE OF INVENTION: WITH HIGH EXPORT YIELD
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

||| |: ||
Db 1 FFLYVLESLP 10

RESULT 8
US-09-328-501-7
; Sequence 7, Application US/09328501A
; Patent No. 6258581
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6258581omu
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: Ceramidase Gene
; FILE REFERENCE: 1422-0377P
; CURRENT APPLICATION NUMBER: US/09/328,501A
; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 10-234769 JAPAN
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-328-501-7

Query Match 41.9%; Score 26; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNV 10
|| |||:
Db 2 FLEVVNI 8

RESULT 9
US-09-777-710A-7
; Sequence 7, Application US/09777710A
; Patent No. 6489117
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6489117omu et al.
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-7

Query Match 41.9%; Score 26; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNV 10
|| |||:
Db 2 FLEVVNI 8

SEQUENCE
US-09-009-953-15

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVNV 10
Db 5 FFLPALPV 12

RESULT 11
US-08-159-339A-1023
; Sequence 1023, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1023:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1023

Query Match 40.3%; Score 25; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVVNVL 11
| | ||::|
Db 2 FLLEVVDIL 10

RESULT 12
US-08-194-981E-16
; Sequence 16, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; TITLE OF INVENTION: CYTOCHROME P450
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-194-981E-16

Query Match 40.3%; Score 25; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFLPVV 8
| ||||:
Db 5 LAVFLPVI 12

RESULT 13
US-09-177-249-88
; Sequence 88, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-88

Query Match 40.3%; Score 25; DB 3; Length 17;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
:||||:
Db 9 WFFLPL 14

RESULT 14
US-08-482-918-94
; Sequence 94, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-482-918-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
|| || |
Db 10 FFMLPPV 16

RESULT 15
US-08-482-918-95
; Sequence 95, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,918
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/33005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FFFLPVV 8
|| || |
Db 10 FFMLPPV 16

RESULT 16
US-09-224-681-94
; Sequence 94, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-681-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
|| || |
Db 10 FFLMLPPV 16

RESULT 17
US-09-224-681-95
; Sequence 95, Application US/09224681
; Patent No. 6207454
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
; TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,681
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,893
; FILING DATE: 12-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/35199
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-681-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
|| || |
Db 10 FFMLPPV 16

RESULT 18
US-08-336-728A-94
; Sequence 94, Application US/08336728A
; Patent No. 6207802
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-336-728A-94

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
|| || |
Db 10 FFMLPPV 16

RESULT 19

US-08-336-728A-95

; Sequence 95, Application US/08336728A
; Patent No. 6207802

; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,728A

;
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-728A-95

Query Match 40.3%; Score 25; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
|| || |
Db 10 FFMLPPV 16

RESULT 20

US-09-103-478-5

; Sequence 5, Application US/09103478

; Patent No. 6235975

; GENERAL INFORMATION:

; APPLICANT: Harada, John

; APPLICANT: Lotan, Tamar

; APPLICANT: Ohto, Masa-aki

; APPLICANT: Goldberg, Robert B.

; APPLICANT: Fischer, Robert L.

; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-103-478-5

Query Match 38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11
:|: ||:
Db 1 MPIANVI 7

RESULT 21
US-09-103-478-17
; Sequence 17, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-077611US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-103-478-17

Query Match 38.7%; Score 24; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
||: ||
Db 1 LPIANV 6

RESULT 22
US-09-193-931C-5
; Sequence 5, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 09/026,221
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 08/804,534
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA binding
; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog with transcription
; OTHER INFORMATION: activation function
US-09-193-931C-5

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11
:|: ||:
Db 1 MPIANVI 7

RESULT 23
US-09-193-931C-17
; Sequence 17, Application US/09193931C
; Patent No. 6320102
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; FILE REFERENCE: 023070-077620
; CURRENT APPLICATION NUMBER: US/09/193,931C
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 09/103,478
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 09/026,221
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: US 08/804,534
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:DNA binding
; OTHER INFORMATION: region of HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF-A) protein yeast homolog
US-09-193-931C-17

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 5 LPVVNV 10
||: ||
Db 1 LPIANV 6

RESULT 24
US-09-026-221-5
; Sequence 5, Application US/09026221
; Patent No. 6545201
; GENERAL INFORMATION:
; APPLICANT: Harada, John J.
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,221
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-077610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-026-221-5

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11
:|: ||:
Db 1 MPIANVI 7

RESULT 25

US-09-026-221-17

; Sequence 17, Application US/09026221
; Patent No. 6545201
; GENERAL INFORMATION:
; APPLICANT: Harada, John J.
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,221
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/804,534
; FILING DATE: 21-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-077610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-026-221-17

Query Match 38.7%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
||: ||
Db 1 LPIANV 6

RESULT 26

US-08-934-222-106

;
; Sequence 106, Application US/08934222
;
; Patent No. 5928896
;
; GENERAL INFORMATION:
;
; APPLICANT: EVANS, Herbert J.
;
; APPLICANT: KINI, R. Manjunatha
;
; TITLE OF INVENTION: Polypeptides That Include Conformation-
;
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
;
; TITLE OF INVENTION: Site
;
; NUMBER OF SEQUENCES: 153
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Foley & Lardner
;
; STREET: Suite 500, 3000 K Street NW
;
; CITY: Washington
;
; STATE: DC
;
; COUNTRY: USA
;
; ZIP: 20007
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/934,222
;
; FILING DATE: 19-SEPT-1997
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 08/532,818
;
; FILING DATE: 03-MAY-1996
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: U.S. 08/143,364
;
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: U.S. 08/051,741
;
; FILING DATE: 23-APR-1993
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Isaacson, John P.
;
; REGISTRATION NUMBER: 33,751
;
; REFERENCE/DOCKET NUMBER: 040433/0148
;
; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-934-222-106

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
| ||||
Db 2 PFGNVLP 8

RESULT 27

US-08-933-402-106

; Sequence 106, Application US/08933402

; Patent No. 5948887

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/933,402

; FILING DATE: 19-SEPT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-933-402-106

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 12
| ||||
Db 2 PFGNVLP 8

RESULT 28

US-09-207-621-106

; Sequence 106, Application US/09207621

; Patent No. 5952465

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein

Interaction Sit

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/207,621

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-106

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 12
| ||||
Db 2 PFGNVLP 8

RESULT 29
US-08-532-818-106
; Sequence 106, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-106

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
 | ||||
Db 2 PFGNVLP 8

RESULT 30
US-09-231-797-106
; Sequence 106, Application US/09231797
; Patent No. 6084066
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction Sit
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-09-231-797-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
| ||||
Db 2 PFGNVL P 8

RESULT 31
US-08-934-224-106
; Sequence 106, Application US/08934224
; Patent No. 6100044
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,224
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-224-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 12
| ||||
Db 2 PFGNVLP 8

RESULT 32
US-08-933-843-106
; Sequence 106, Application US/08933843
; Patent No. 6111069
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,843
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-843-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL P 12
| ||||
Db 2 PFGNVLP 8

RESULT 33
US-08-934-223-106
; Sequence 106, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-223-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVNVLP 12
| ||||
Db 2 PFGNVLP 8

RESULT 34
US-09-413-492-106
; Sequence 106, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-106

Query Match 38.7%; Score 24; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 12
| ||||
Db 2 PFGNVL 8

RESULT 35

US-10-118-575A-7

; Sequence 7, Application US/10118575A
; Patent No. 6653443
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Hui
; APPLICANT: PONERANZ, Roger
; APPLICANT: YANG, Bin
; TITLE OF INVENTION: Multimerization of HIV-1 VIF Protein as
; TITLE OF INVENTION: a Therapeutic Target
; FILE REFERENCE: 8321-82 PC
; CURRENT APPLICATION NUMBER: US/10/118,575A
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/282,270
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide containing PXP motif

US-10-118-575A-7

Query Match 38.7%; Score 24; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLPV 7
:||||
Db 6 YFLPV 10

RESULT 36

PCT-US94-10257A-16

; Sequence 16, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK

; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-16

Query Match 38.7%; Score 24; DB 5; Length 13;
Best Local Similarity 45.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFF LPVV NVL 11
|| :||: |
Db 3 LFVIV PVL GPL 13

RESULT 37
US-08-213-419B-7
; Sequence 7, Application US/08213419B
; Patent No. 6333406
; GENERAL INFORMATION:
; APPLICANT: Inselburg, J. et al.
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: JII-002CNCP

; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-08-213-419B-7

Query Match 38.7%; Score 24; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFILPVV 8
||| | |:
Db 7 LFFILCVI 14

RESULT 38
US-08-559-492-10
; Sequence 10, Application US/08559492
; Patent No. 5843884
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
; TITLE OF INVENTION: C9 Complement Inhibitor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; STREET: Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,492
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-873-8794
; TELEFAX: 404-873-8795
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-559-492-10

Query Match 37.1%; Score 23; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPVV 8
||| ::
Db 1 FFFLKLL 7

RESULT 39
US-09-171-337A-17
; Sequence 17, Application US/09171337A
; Patent No. 6300095
; GENERAL INFORMATION:
; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE, Migueul Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/4" Disk 1.44MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,337A
; FILING DATE: 14-May-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ES98/00056
; FILING DATE: 5-MAR-1998
; APPLICATION NUMBER: ES9700482
; FILING DATE: 5-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, Clifford J.
; REGISTRATION NUMBER: 30,086
; (C) REF./DOCKET NO.: U-011948-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 233288

; INFORMATION FOR SEQ ID NO: 17
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Penicillum chrysogenum
; SEQUENCE DESCRIPTION: SEQ ID NO: 17
US-09-171-337A-17

Query Match 37.1%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FLPVVNVL 11
| :|||
Db 1 FASVLNVL 8

RESULT 40

US-09-631-022-17

; Sequence 17, Application US/09631022

; Patent No. 6558921

; GENERAL INFORMATION:

; APPLICANT: BARREDO FUENTE, Jose Luis
; RODRIGUEZ SAIZ, Marta
; COLLADOS DE LA VIEJA, Alfonso J.
; MORENO VALLE, Migueul Angel
; SALTO MALDONADO, Francisco
; DIEZ GARCIA, Bruno

; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
; AND -ACTIN AND THEIR USE IN FILAMENTOUS
; FUNGI EXPRESSION, SECRETION AND ANTISENSE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61 STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10023

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3-1/4" Disk 1.44MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
; SOFTWARE: WordPerfect 8 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/631,022
; FILING DATE: 02-Aug-2000
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/171,337
; FILING DATE: 14-MAY-1999
; APPLICATION NUMBER: PCT/ES98/00056
; FILING DATE: 5-MAR-1998

APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
(C) REF./DOCKET NO.: U-02886-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
SEQUENCE DESCRIPTION: SEQ ID NO: 17
US-09-631-022-17

Query Match 37.1%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 FLPVVNL 11
| :|||
Db 1 FASVLNVL 8

RESULT 41
US-08-979-847B-150
; Sequence 150, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC,
PROPHYLACTIC AND
; THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,847B
; FILING DATE: 26-No. 6582703-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 39046A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-08-979-847B-150

Query Match 37.1%; Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
|| :||
Db 3 FFCIPV 8

RESULT 42
US-08-979-847B-151
; Sequence 151, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC,
PROPHYLACTIC AND
; THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA

ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 151:
US-08-979-847B-151

Query Match 37.1%; Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 FFFLPV 7
|| :||
Db 2 FFCIPV 7

RESULT 43
US-08-979-847B-152
; Sequence 152, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC,
PROPHYLACTIC AND
; THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC

;
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,847B
; FILING DATE: 26-No. 6582703-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 39046A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 152:
US-08-979-847B-152

Query Match 37.1%; Score 23; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FFLPV 7
|| :||
Db 1 FFCIPV 6

RESULT 44
US-08-159-339A-1217
; Sequence 1217, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1217

Query Match 37.1%; Score 23; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FFLPVV 8
:| ||:
Db 1 YFFPVI 6

RESULT 45
US-08-159-339A-1218
; Sequence 1218, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1218

Query Match 37.1%; Score 23; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVV 8
:| ||:
Db 4 YFFPVI 9

RESULT 46
US-09-492-543-149
; Sequence 149, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-B

; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 149
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 62-70 of the PUMP-1 protein
US-09-492-543-149

Query Match 37.1%; Score 23; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 FFFLPV 7
|| ||:
Db 4 FFGLPI 9

RESULT 47
US-09-492-543-159
; Sequence 159, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 62-70 of the PUMP-1 protein
US-09-492-543-159

Query Match 37.1%; Score 23; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 FFFLPV 7
|| ||:
Db 4 FFGLPI 9

RESULT 48
US-09-527-487-5

; Sequence 5, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-487-5

Query Match 37.1%; Score 23; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FFFLPVVNV 10
| | | : |
Db 1 FLFTPPTIYV 9

RESULT 49
US-08-159-339A-1219
; Sequence 1219, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746

;
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1219

Query Match 37.1%; Score 23; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVV 8
:| ||:
Db 4 YFFPVI 9

RESULT 50
US-08-508-664-13
; Sequence 13, Application US/08508664
; Patent No. 5840542
; GENERAL INFORMATION:
; APPLICANT: KANG, Yup
; APPLICANT: YOON, Ji-Won
; TITLE OF INVENTION: METHOD FOR MANUFACTURE OF PROINSULIN
; TITLE OF INVENTION: WITH HIGH EXPORT YIELD
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,664
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter

;
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0136/0B300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: CONN PEPTIDE
US-08-508-664-13

Query Match 37.1%; Score 23; DB 2; Length 11;
Best Local Similarity 30.0%; Pred. No. 6.5e+02;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FFFLPVVNVL 11
||: | ::
Db 1 FFYTPKTGIV 10

Search completed: July 4, 2004, 04:48:47
Job time : 8.52239 secs

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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 9.22388 Seconds
(without alignments)
125.142 Million cell updates/sec

Title: US-09-641-802-4

Perfect score: 62

Sequence: 1 LFFFLLPVVNVL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query Score	Match	Length	DB	ID	Description
1	23	37.1	16	2	T37075	hypothetical prote
2	22	35.5	18	2	S53125	cysteine-rich secr
3	21	33.9	13	2	JZVHP1	crabolin - Europe
4	21	33.9	13	2	S09019	hemolytic protein
5	21	33.9	14	2	JN0390	histamine-releasin
6	21	33.9	14	2	S62374	alpha-1-antichymot
7	21	33.9	17	2	S15778	insulin chain B -
8	21	33.9	18	2	S09731	photosystem I prot
9	21	33.9	18	2	I40062	shikimate 5-dehydr
10	20	32.3	9	2	S66636	alpha-2-macroglobu
11	20	32.3	10	2	S65715	aryl hydrocarbon (
12	20	32.3	13	2	S09018	hemolytic protein
13	20	32.3	15	2	AF0832	phe leader peptide

14	20	32.3	18	2	A39040	calsequestrin, car
15	19.5	31.5	18	2	S04229	N4-(beta-N-acetylgl
16	19	30.6	13	2	S01119	photosystem II pro
17	19	30.6	13	4	I70076	glycophorin B/glyc
18	19	30.6	15	2	PA0029	protein QA100012 -
19	19	30.6	15	2	S13973	chlorophyll a/b-bi
20	19	30.6	15	2	S54712	zein Zp22/6 protei
21	19	30.6	16	2	T09741	photosystem I chai
22	19	30.6	16	2	T44936	calmodulin kinase
23	19	30.6	17	2	C37520	glutathione transf
24	19	30.6	18	2	S70612	alpha-macroglobuli
25	18.5	29.8	17	2	JQ2030	hypothetical 1.9K
26	18	29.0	14	1	LFECFS	pheST operon leade
27	18	29.0	14	2	A60737	pollen allergen Lo
28	18	29.0	14	2	AF0296	phenylalanyl-tRNA
29	18	29.0	14	2	F90931	pheST operon leade
30	18	29.0	14	2	B85780	pheST operon leade
31	18	29.0	14	2	AG0705	phenylalanyl-tRNA
32	18	29.0	15	1	LFECF	phe operon leader
33	18	29.0	15	2	E91061	hypothetical prote
34	18	29.0	15	2	PS0185	27K protein A 3.4/
35	18	29.0	15	2	A36279	chemoattractant pr
36	18	29.0	15	2	S71306	heat shock protein
37	18	29.0	16	2	S11290	matrix protein M1
38	18	29.0	16	2	S68730	bleomycin-binding
39	18	29.0	17	2	E23734	insulin-like growt
40	18	29.0	18	2	A32220	T-cell receptor de
41	18	29.0	18	2	I50389	myosin heavy chain
42	18	29.0	18	4	I54078	hypothetical PML/R
43	17	27.4	8	2	B24749	neuropeptide B - b
44	17	27.4	10	2	D28027	protein P7 - curle
45	17	27.4	10	2	S68033	cytochrome P450 1A
46	17	27.4	11	2	B59146	conotoxin au5b - c
47	17	27.4	12	2	I40663	bma protein - Clos
48	17	27.4	14	2	S50900	chlorophyll a/b-bi
49	17	27.4	14	2	S27140	hypothetical prote
50	17	27.4	14	2	S58862	botulinum neurotox
51	17	27.4	14	2	S58866	botulinum neurotox
52	17	27.4	14	2	PH1614	Ig H chain V-D-J r
53	17	27.4	15	2	PQ0750	self-incompatibili
54	17	27.4	15	2	A36315	recycling receptor
55	17	27.4	15	2	PN0665	dystrophin-associa
56	17	27.4	16	2	A42291	tail fiber protein
57	17	27.4	16	2	G45681	orf 61.1 - phage T
58	17	27.4	16	2	S01104	hypothetical prote
59	17	27.4	17	2	S05913	chorion class A pr
60	17	27.4	17	2	E22595	bombolitin V - Ame
61	17	27.4	18	2	S39153	translation elonga
62	17	27.4	18	2	A30541	F7-1 fimbrial prot
63	17	27.4	18	2	A42016	mammary-derived gr
64	16	25.8	9	2	S13636	coat protein beta
65	16	25.8	9	2	D48186	ATPase R1 subunit
66	16	25.8	10	2	D46285	formaldehyde dehyd
67	16	25.8	10	2	PT0251	Ig heavy chain CRD
68	16	25.8	10	2	B61218	alpha-gliadin 6Ha
69	16	25.8	11	2	D61033	ranatachykinin D -
70	16	25.8	11	2	S69349	neuropeptide FFam

71	16	25.8	12	1	LFECPE	pyrE leader peptid
72	16	25.8	12	2	S26555	T-cell receptor be
73	16	25.8	12	2	S26556	T-cell receptor be
74	16	25.8	12	2	S26554	T-cell receptor be
75	16	25.8	13	2	S47371	T-cell antigen rec
76	16	25.8	13	2	S47390	T-cell antigen rec
77	16	25.8	14	2	S29632	xylan 1,4-beta-xyl
78	16	25.8	14	2	I39753	nitrogenase (EC 1.
79	16	25.8	14	2	A60158	disaggregatase - M
80	16	25.8	15	2	PQ0195	Sf11-glycoprotein
81	16	25.8	15	2	PA0105	heat shock protein
82	16	25.8	15	2	A61612	allatostatin - tob
83	16	25.8	15	2	PT0205	insulin-like growt
84	16	25.8	15	2	S57577	T cell receptor V-
85	16	25.8	16	2	A36300	T-cell receptor ga
86	16	25.8	16	2	I40065	shikimate 5-dehydr
87	16	25.8	16	2	B24099	crystal protein, 7
88	16	25.8	16	2	S09732	photosystem I prot
89	16	25.8	16	2	G49039	T-cell receptor be
90	16	25.8	16	2	H49039	T-cell receptor be
91	16	25.8	16	2	G24687	T-cell receptor be
92	16	25.8	16	2	A28587	T-cell receptor be
93	16	25.8	16	2	B60566	cytochrome P450m51
94	16	25.8	16	2	PH1476	T-cell receptor be
95	16	25.8	16	2	PH1475	T-cell receptor be
96	16	25.8	16	2	PH1474	T-cell receptor be
97	16	25.8	16	2	PH1472	T-cell receptor be
98	16	25.8	16	2	PH1477	T-cell receptor be
99	16	25.8	16	2	PH1473	T-cell receptor be
100	16	25.8	16	2	PH0766	T-cell receptor be

ALIGNMENTS

RESULT 1

T37075

hypothetical protein SCJ30.08 - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T37075

R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.;

Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21621

A;Accession: T37075

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-16 <SAN>

A;Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070;

SCOEDB:SCJ30.08

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCJ30.08

Query Match 37.1%; Score 23; DB 2; Length 16;
 Best Local Similarity 37.5%; Pred. No. 7.7e+02;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 5 LPVVNVLP 12
:||: :|
Db 1 MPVIRSMP 8

RESULT 2
S53125
cysteine-rich secretory protein-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S53125; S56161
R;Schwidetzky, U.; Haendler, B.; Schleuning, W.D.
submitted to the EMBL Data Library, March 1995
A;Description: Isolation and characterization of the androgen-dependent mouse
cysteine-rich secretory protein-3 (CRISP-3) gene.
A;Reference number: S53125
A;Accession: S53125
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <SCH>
A;Cross-references: EMBL:X85321
R;Schwidetzky, U.; Haendler, B.; Schleuning, W.D.
Biochem. J. 309, 831-836, 1995
A;Title: Isolation and characterization of the androgen-dependent mouse
cysteine-rich secretory protein-3 (CRISP-3) gene.
A;Reference number: S56161; MUID:95366959; PMID:7639699
A;Accession: S56161
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <SC2>
A;Cross-references: EMBL:X85321

Query Match 35.5%; Score 22; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 FFFL 5
||||
Db 4 FFFL 7

RESULT 3
JZVHP1
crabrolin - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A01781
R;Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A;Title: Isolation and characterization of two new peptides, mastoparan C and
crabrolin, from the venom of the European hornet, Vespa crabro.
A;Reference number: A92441; MUID:84289390; PMID:6206053
A;Accession: A01781
A;Molecule type: protein
A;Residues: 1-13 <ARG>

C;Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; venom

F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 33.9%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPLI 5

RESULT 4

S09019

hemolytic protein B9 - edible frog (fragment)

C;Species: Rana esculenta (edible frog)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993

C;Accession: S09019

R;Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.; Bossa, F.

Biochim. Biophys. Acta 1033, 318-323, 1990

A;Title: Purification and characterization of bioactive peptides from skin extracts of Rana esculenta.

A;Reference number: S09018; MUID:90198965; PMID:2317508

A;Accession: S09019

A;Molecule type: protein

A;Residues: 1-13 <SIM>

Query Match 33.9%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPLI 5

RESULT 5

JN0390

histamine-releasing peptide II - oriental hornet

N;Alternate names: venom protein HR-2

C;Species: Vespa orientalis (oriental hornet)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997

C;Accession: JN0390; S10919

R;Miroshnikov, A.I.; Snejzhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gushchin, I.S.

Bioorg. Khim. 7, 1467-1477, 1981

A;Title: Structure and properties of histamine releasing peptides from the venom of Vespa orientalis hornet.

A;Reference number: JN0389

A;Accession: JN0390

A;Molecule type: protein

A;Residues: 1-14 <MIR>

R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. Structure and function.
A;Reference number: S06445
A;Accession: S10919
A;Molecule type: protein
A;Residues: 1-14 <TUI>
C;Superfamily: crabrolin
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 33.9%; Score 21; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPLI 5

RESULT 6
S62374
alpha-1-antichymotrypsin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
C;Accession: S62374
R;Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.;
Tsuda, T.; Tachikawa, H.; Yamamoto, M.; Shinohara, Y.
Eur. J. Biochem. 235, 821-827, 1996
A;Title: The defective secretion of a naturally occurring alpha-1-
antichymotrypsin variant with a frameshift mutation.
A;Reference number: S62374; MUID:96184564; PMID:8654434
A;Accession: S62374
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14 <TSU>

Query Match 33.9%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVN 9
:|||
Db 2 IFFMSKVTN 10

RESULT 7
S15778
insulin chain B - bovine (fragments)
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: S15778; S15779
R;Bergman, T.; Agerberth, B.; Joernvall, H.
FEBS Lett. 283, 100-103, 1991

A;Title: Direct analysis of peptides and amino acids from capillary electrophoresis.

A;Reference number: S15778; MUID:91243852; PMID:2037061

A;Accession: S15778

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <FEB1>

A;Accession: S15779

A;Status: preliminary

A;Molecule type: protein

A;Residues: 9-17 <FEB2>

C;Superfamily: insulin

C;Keywords: hormone; pancreas

Query Match 33.9%; Score 21; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6
||: |
Db 11 FFYTP 15

RESULT 8

S09731

photosystem I protein psaI - spinach chloroplast (fragment)

C;Species: chloroplast Spinacia oleracea (spinach)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996

C;Accession: S09731

R;Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.

FEBS Lett. 263, 274-278, 1990

A;Title: Polypeptide composition of higher plant photosystem I complex.

Identification of psaI, psaJ and psaK gene products.

A;Reference number: S09730; MUID:90242987; PMID:2185953

A;Accession: S09731

A;Molecule type: protein

A;Residues: 1-18 <IKE>

C;Genetics:

A;Gene: psaI

A;Genome: chloroplast

C;Superfamily: photosystem I protein psaI

C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; thylakoid

Query Match 33.9%; Score 21; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.9e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNV 11
|:|:| ::
Db 7 FVPLVGLV 14

RESULT 9

I40062

shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)

C;Species: Buchnera aphidicola

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40062
R;Rouhbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera
aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding gene.
A;Reference number: I40061; MUID:95212914; PMID:7535281
A;Accession: I40062
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18 <RES>
A;Cross-references: EMBL:U10496; NID:g854711; PIDN:AAA79125.1; PID:g854712
C;Genetics:
A;Gene: aroE
C;Keywords: oxidoreductase

Query Match 33.9%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
||||
Db 7 NVLP 10

RESULT 10
S66636
alpha-2-macroglobulin isoform 2 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
C;Accession: S66636
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup,
S.; Sottrup-Jensen, L.; Nyborg, J.
FEBS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding
domain of human and bovine alpha(2)-macroglobulin.
A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66636
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DOL>

Query Match 32.3%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NVLP 12
|:||
Db 2 NILP 5

RESULT 11
S65715
aryl hydrocarbon (benzo[a]pyrene) hydroxylase (EC 1.14.14.-) cytochrome P450
K(Ah) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 29-Oct-1999

C;Accession: S65715
R;Ohgiya, N.; Yokota, H.; Takahashi, M.; Komoro, S.; Yuasa, A.
Biochim. Biophys. Acta 1289, 122-130, 1996
A;Title: Purification and properties of a new beta-naphthoflavone inducible
cytochrome P-450, aryl hydrocarbon hydroxylase from rat kidney.
A;Reference number: S65715; MUID:96195850; PMID:8605221
A;Accession: S65715
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <OHG>
C;Keywords: monooxygenase; oxidoreductase

Query Match 32.3%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVVNVLP 12
:|| :||
Db 3 VPVXLLLP 10

RESULT 12
S09018
hemolytic protein A1 - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S09018
R;Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erspamer, G.F.; Barra, D.;
Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A;Title: Purification and characterization of bioactive peptides from skin
extracts of Rana esculenta.
A;Reference number: S09018; MUID:90198965; PMID:2317508
A;Accession: S09018
A;Molecule type: protein
A;Residues: 1-13 <SIM>

Query Match 32.3%; Score 20; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPAI 5

RESULT 13
AF0832
phe leader peptide [imported] - *Salmonella enterica* subsp. *enterica* serovar
Typhi (strain CT18)
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0832
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.;
Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker,
S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis,

P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
A;Title: Complete genome sequence of a multiple drug resistant *Salmonella* enterica serovar Typhi CT18.
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0832
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05845.1; PID:g16503820; GSPDB:GN00176
C;Genetics:
A;Gene: STY2853a

Query Match 32.3%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5
|||:
Db 10 FFFI 13

RESULT 14
A39040
calsequestrin, cardiac muscle - dog (fragments)
C;Species: *Canis lupus familiaris* (dog)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: A39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein kinase II. Demonstration of a cluster of unique rapidly phosphorylated sites in cardiac calsequestrin.
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: A39040
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <CAL>
C;Keywords: cardiac muscle; heart; phosphoprotein

Query Match 32.3%; Score 20; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNV 9
|| :|
Db 8 LPTIN 12

RESULT 15
S04229
N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)

N;Alternate names: glycosylasparaginase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C;Accession: S04229
R;Tollersrud, O.K.; Aronson Jr., N.N.
Biochem. J. 260, 101-108, 1989
A;Title: Purification and characterization of rat liver glycosylasparaginase.
A;Reference number: S04228; MUID:89374025; PMID:2775174
A;Accession: S04229
A;Molecule type: protein
A;Residues: 1-18 <TOL>
C;Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase
C;Keywords: hydrolase

Query Match 31.5%; Score 19.5; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 5 LP-VVNVL 12
|| || |
Db 4 LPLVVNTWP 12

RESULT 16
S01119
photosystem II protein psbK - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1996
C;Accession: S01119
R;Murata, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugiura, M.
FEBS Lett. 235, 283-288, 1988
A;Title: Identification of a new gene in the chloroplast genome encoding a low-molecular-mass polypeptide of photosystem II complex.
A;Reference number: S01119
A;Accession: S01119
A;Molecule type: protein
A;Residues: 1-13 <MUR>
C;Genetics:
A;Gene: psbK
A;Genome: chloroplast
C;Superfamily: photosystem II protein psbK
C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; thylakoid

Query Match 30.6%; Score 19; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVV 8
| |:|
Db 8 FLXPIV 13

RESULT 17
I70076
glycophorin B/glycophorin A mutant fusion protein St-a (mistranslated) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000
C;Accession: I70076
R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.
J. Biol. Chem. 265, 9259-9263, 1990
A;Title: Identification of the crossing-over point of a hybrid gene encoding
human glycophorin variant St-a: Similarity to the crossing-over point in
haptoglobin-related genes.
A;Reference number: I55334; MUID:90264417; PMID:1971625
A;Accession: I70076
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-13 <REA>
A;Cross-references: GB:M33507; GB:J05465; NID:g183743; PIDN:AAA35942.1;
PID:g442426
A;Note: the translation is from an incorrect reading frame
C;Genetics:
A;Gene: GYPB/GYPA
C;Keywords: fusion protein

Query Match 30.6%; Score 19; DB 4; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
||:::
Db 6 LPIISL 11

RESULT 18
PA0029
protein QA100012 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0029
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-
dimensional gel electrophoresis.
A;Reference number: PA0001
A;Accession: PA0029
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: callus

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.6e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 FLPVVNVLP 12
| ||| |
Db 7 FTLVVNNXP 15

RESULT 19
S13973
chlorophyll a/b-binding protein type II - garden pea (fragment)

C;Species: Pisum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S13973
R;Jahns, P.; Junge, W.
Eur. J. Biochem. 193, 731-736, 1990
A;Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the proton-pumping activity of photosystem II. Identified as light-harvesting chlorophyll-a/b-binding proteins.
A;Reference number: S13973; MUID:91065379; PMID:2174365
A;Accession: S13973
A;Molecule type: protein
A;Residues: 1-15 <JAH>
C;Genetics:
A;Genome: nuclear
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; thylakoid; transmembrane protein

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFLLPVNV 10
:| : ::||
Db 5 VFTSIGIINV 14

RESULT 20
S54712
zein Zp22/6 protein - maize
C;Species: Zea mays (maize)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: S54712
R;Chaudhuri, S.; Messing, J.
Mol. Genet. 246, 707-715, 1995
A;Title: RFLP mapping of the maize dzrl locus, which regulates methionine-rich 10 kDa zein accumulation.
A;Reference number: S54712; MUID:95206245; PMID:7898438
A;Accession: S54712
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <CHA>

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 FFLPVNVNLP 12
| :| :: |
Db 1 FIIIPQQSLAP 10

RESULT 21
T09741
photosystem I chain psaI - upland cotton chloroplast (fragment)
C;Species: chloroplast Gossypium hirsutum (upland cotton)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T09741

R;Small, R.L.; Ryburn, J.A.; Cronn, R.C.; Seelanan, T.; Wendel, J.F.
Am. J. Bot. 85, 1301-1315, 1998
A;Title: The tortoise and the hare: choosing between noncoding plastome and
nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant
group.
A;Reference number: Z16323
A;Accession: T09741
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <SMA>
A;Cross-references: EMBL:AF031581; NID:g2623684; PID:g3723945
C;Genetics:
A;Gene: psaI
A;Genome: chloroplast
C;Keywords: chloroplast; photosynthesis; photosystem I

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|:|:
Db 11 FVPLV 15

RESULT 22
T44936
calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T44936
R;Alemany, V.; Aligue, R.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z22873
A;Accession: T44936
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-16 <ALE>
A;Cross-references: EMBL:U57982; PIDN:AAD09466.1

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVN 9
|| || |
Db 10 FFTVVTN 16

RESULT 23
C37520
glutathione transferase (EC 2.5.1.18) MII - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 30-Sep-1993
C;Accession: C37520; N24735
R;Mannervik, B.; Alin, P.; Guthenberg, C.; Jensson, H.; Tahir, M.K.; Warholm, M.; Jornvall, H.

Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985

A;Title: Identification of three classes of cytosolic glutathione transferase common to several mammalian species: correlation between structural data and enzymatic properties.

A;Reference number: A24735; MUID:86042634; PMID:3864155

A;Accession: C37520

A;Molecule type: protein

A;Residues: 1-17 <MAN>

C;Superfamily: glutathione transferase

C;Keywords: transferase

Query Match 30.6%; Score 19; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVNV 9
: |||:
Db 7 YFPVVD 12

RESULT 24

S70612

alpha-macroglobulin proteinase inhibitor, tetrameric - bloodfluke planorb (fragment)

C;Species: Biomphalaria glabrata (bloodfluke planorb)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C;Accession: S70612

R;Bender, R.C.; Bayne, C.J.

Biochem. J. 316, 893-900, 1996

A;Title: Purification and characterization of a tetrameric alpha-macroglobulin proteinase inhibitor from the gastropod mollusc Biomphalaria glabrata.

A;Reference number: S70612; MUID:96265058; PMID:8670168

A;Accession: S70612

A;Molecule type: protein

A;Residues: 1-18 <BEN>

C;Complex: homotetramer

C;Function:

A;Description: inhibits proteinases possessing different catalytic mechanisms by steric shielding of the active site from large substrates; trap mechanism

Query Match 30.6%; Score 19; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 FFFLPVNVLP 12
:| ||:|
Db 3 YFISAPRNVP 13

RESULT 25

JQ2030

hypothetical 1.9K protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

N;Alternate names: ORF2 mini gene protein

C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999

C;Accession: JQ2030

R; Russell, R.L.Q.; Rohrmann, G.F.
J. Gen. Virol. 74, 1191-1195, 1993
A; Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.
A; Reference number: PQ0633; MUID:93286576; PMID:8389803
A; Accession: JQ2030
A; Molecule type: DNA
A; Residues: 1-17 <RUS>
A; Cross-references: DDBJ:D13375; NID:g222217; PIDN:BAA02640.1; PID:d1003144;
PID:g222222

Query Match 29.8%; Score 18.5; DB 2; Length 17;
Best Local Similarity 85.7%; Pred. No. 5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 5 LPVVNL 11
|| ||||
Db 3 LP-VNVL 8

RESULT 26
LFECFS
pheST operon leader peptide - Escherichia coli (strain K-12)
N; Alternate names: phenylalanyl-tRNA synthetase operon leader peptide
C; Species: Escherichia coli
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Mar-2002
C; Accession: S11551; I53984; C64930; S06908
R; Fayat, G.; Mayaux, J.F.; Sacerdot, C.; Fromant, M.; Springer, M.; Grunberg-Manago, M.; Blanquet, S.
J. Mol. Biol. 171, 239-261, 1983
A; Title: Escherichia coli phenylalanyl-tRNA synthetase operon region. Evidence for an attenuation mechanism. Identification of the gene for the ribosomal protein L20.
A; Reference number: A30391; MUID:84090239; PMID:6317865
A; Accession: S11551
A; Molecule type: DNA
A; Residues: 1-14 <FAY>
A; Cross-references: EMBL:V00291; NID:g43065; PIDN:CAA23563.1; PID:g43069
R; Mayaux, J.
Gene 30, 137-146, 1984
A; Title: IS4 transposition in the attenuator region of the Escherichia coli pheS,T operon.
A; Reference number: I53984; MUID:85077605; PMID:6096210
A; Accession: I53984
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-14 <RES>
A; Cross-references: GB:M13251; NID:g147182; PIDN:AAA24333.1; PID:g147185
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: C64930
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA

A;Residues: 1-14 <BLAT>
A;Cross-references: GB:AE000266; GB:U00096; NID:g1787997; PIDN: AAC74785.1;
PID:g1788008; UWGP:b1715
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: pheM
A;Map position: 37 min
C;Function:
A;Description: probably involved in attenuation regulation of phenylalanyl-tRNA synthetase operon
C;Superfamily: pheST leader peptide

Query Match 29.0%; Score 18; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
 |||
Db 8 FFF 10

RESULT 27
A60737
pollen allergen Lol p IV - perennial ryegrass (fragments)
C;Species: Lolium perenne (perennial ryegrass)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 17-Mar-1999
C;Accession: A60737
R;Jaggi, K.S.; Ekramoddoullah, A.K.M.; Kisil, F.T.
Int. Arch. Allergy Appl. Immunol. 89, 342-348, 1989
A;Title: Allergenic fragments of ryegrass (Lolium perenne) pollen allergen Lol p IV.
A;Reference number: A60737; MUID:90007726; PMID:2793222
A;Accession: A60737
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <JAG>
C;Keywords: pollen

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 5e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVNVL 11
 | ||: ::
Db 1 FLEPVVLGLI 9

RESULT 28
AF0296
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0296
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.;
Prentice, M.B.; Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker,
S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth,

T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0296

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-14 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC91234.1; PID:g15980423; GSPDB:GN00175

C;Genetics:

A;Gene: pheM

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 8 FFF 10

RESULT 29

F90931

pheST operon leader peptide - *Escherichia coli* (strain O157:H7, substrain RIMD 0509952)

C;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001

C;Accession: F90931

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F90931

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-14 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAB35845.1; PID:g13361889; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs2422

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 8 FFF 10

RESULT 30
B85780
pheST operon leader peptide - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: B85780
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85780
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <STO>
A;Cross-references: GB:AE005174; NID:g12515726; PIDN:AAG56702.1; GSPDB:GN00145; UWGP:Z2744
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: pheM

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 8 FFF 10

RESULT 31
AG0705
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0705
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0705
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-14 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02016.1; PID:g16502854; GSPDB:GN00176
C;Genetics:
A;Gene: STY1774

Query Match 29.08; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 8 FFF 10

RESULT 32
LFECF
phe operon leader peptide - Escherichia coli (strain K-12)
N;Alternate names: attenuator peptide
C;Species: Escherichia coli
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 01-Mar-2002
C;Accession: A03593; B36494; A65038
R;Zurawski, G.; Brown, K.; Killingly, D.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 75, 4271-4275, 1978
A;Title: Nucleotide sequence of the leader region of the phenylalanine operon of Escherichia coli.
A;Reference number: A03593; MUID:79033820; PMID:360214
A;Accession: A03593
A;Molecule type: DNA
A;Residues: 1-15 <ZUR>
A;Cross-references: GB:V00314; GB:J01658; NID:g42378; PIDN:CAA23600.1;
PID:g42379
R;Gavini, N.; Davidson, B.E.
J. Biol. Chem. 265, 21532-21535, 1990
A;Title: pheAo mutants of Escherichia coli have a defective pheA attenuator.
A;Reference number: A36494; MUID:91072346; PMID:2254312
A;Accession: B36494
A;Molecule type: DNA
A;Residues: 1-15 <GAV>
A;Cross-references: GB:M58024; GB:J05694; NID:g147178; PIDN:AAA62783.1;
PID:g147180
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.;
Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65038
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-15 <BLAT>
A;Cross-references: GB:AE000346; GB:U00096; NID:g2367141; PIDN: AAC75647.1;
PID:g1788950; UWGP:b2598
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: pheL; pheAe
A;Map position: 56 min
C;Superfamily: pheA leader peptide

Query Match 29.0%; Score 18; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 6 FFF 8

RESULT 33
E91061
hypothetical protein ECs3461 [imported] - Escherichia coli (strain O157:H7,
substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: E91061
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;
Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida,
T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara,
S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
and genomic comparison with a laboratory strain K-12.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36884.1; PID:g13362932; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3461

Query Match 29.0%; Score 18; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 6 FFF 8

RESULT 34
PS0185
27K protein A 3.4/5 - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C;Accession: PS0185
R;Kamo, M.; Tsugita, A.
submitted to JIPID, June 1991
A;Reference number: PS0184
A;Accession: PS0185
A;Molecule type: protein
A;Residues: 1-15 <KAM>

Query Match 29.0%; Score 18; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 VVNVL 12
:|:| |
Db 5 IVDVAP 10

RESULT 35

A36279

chemoattractant protein - earthworm (*Lumbricus terrestris*) (fragment)

C;Species: *Lumbricus terrestris* (common earthworm)

C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993

C;Accession: A36279

R;Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990

A;Title: Purification and characterization of a chemoattractant from electric shock-induced earthworm secretion, its receptor binding, and signal transduction through the vomeronasal system of garter snakes.

A;Reference number: A36279; MUID:90256800; PMID:2160465

A;Accession: A36279

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <JIA>

Query Match 29.0%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| :||
Db 8 FTYLP 12

RESULT 36

S71306

heat shock protein 90 - rat (fragment)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S71306

R;Conconi, M.; Szweda, L.I.; Levine, R.L.; Stadtman, E.R.; Friguet, B.

Arch. Biochem. Biophys. 331, 232-240, 1996

A;Title: Age-related decline of rat liver multicatalytic proteinase activity and protection from oxidative inactivation by heat-shock protein 90.

A;Reference number: S71306; MUID:96299287; PMID:8660703

A;Accession: S71306

A;Molecule type: protein

A;Residues: 1-15 <CON>

A;Experimental source: liver

C;Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 29.0%; Score 18; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 11
|:| |

Db 9 PIVETL 14

RESULT 37

S11290

matrix protein M1 - influenza A virus (strain A/FPV/Rostock/34 [H7N1])

(fragment)

C;Species: influenza A virus

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1993

C;Accession: S11290

R;Robertson, J.S.

Nucleic Acids Res. 6, 3745-3757, 1979

A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza virus.

A;Reference number: S11286; MUID:80034428; PMID:493121

A;Accession: S11290

A;Molecule type: genomic RNA

A;Residues: 1-16 <ROB>

A;Cross-references: EMBL:J02112

C;Genetics:

A;Map position: segment 7

C;Superfamily: influenza virus matrix protein M1

Query Match 29.0%; Score 18; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNVL 12

||:||:|

Db 11 VLSVVP 16

RESULT 38

S68730

bleomycin-binding protein - Streptomyces verticillus (fragment)

C;Species: Streptomyces verticillus

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999

C;Accession: S68730

R;Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakamura, N.; Davies, J.E.

FEBS Lett. 362, 80-84, 1995

A;Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Streptomyces verticillus and a methicillin-resistant Staphylococcus aureus in Escherichia coli and their immunological characterisation.

A;Reference number: S68730; MUID:95212588; PMID:7535252

A;Accession: S68730

A;Molecule type: protein

A;Residues: 1-16 <SUG>

A;Experimental source: ATCC 15003

C;Keywords: antibiotic resistance

Query Match 29.0%; Score 18; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 5.8e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FLPVVNL 11

|| | ||

Db 4 FLGAVPVL 11

RESULT 39

E23734

insulin-like growth factor-binding protein 3 - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993

C;Accession: E23734

R;Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.

Mol. Endocrinol. 5, 938-948, 1991

A;Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6.

A;Reference number: A23734; MUID:92049376; PMID:1719383

A;Accession: E23734

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <SHI>

Query Match 29.0%; Score 18; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 6.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 PVVNVL 12

||| |

Db 9 PVVRXEP 15

RESULT 40

A32220

T-cell receptor delta chain precursor V region (DN7.3-1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 30-May-1997

C;Accession: A32220

R;Korman, A.J.; Maruyama, J.; Raulet, D.H.

Proc. Natl. Acad. Sci. U.S.A. 86, 267-271, 1989

A;Title: Rearrangement by inversion of a T-cell receptor delta variable region gene located 3' of the delta constant region gene.

A;Reference number: A32220; MUID:89098895; PMID:2789518

A;Accession: A32220

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-18 <KOR>

A;Cross-references: GB:M23095

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 29.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4

|||

Db 9 FFF 11

RESULT 41

I50389
myosin heavy chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50389
R;Freyer, G.A.; Robbins, J.
J. Biol. Chem. 258, 7149-7154, 1983
A;Title: the analysis of a chicken myosin heavy chain cdna clone.
A;Reference number: I50388; MUID:83213464; PMID:6304080
A;Accession: I50389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-18 <FRE>
A;Cross-references: GB:K00815; NID:g212369; PIDN:AAA48969.1; PID:g212370

Query Match 29.0%; Score 18; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVVNV 10
| || :|:
Db 4 LMLFLLCLNL 13

RESULT 42
I54078
hypothetical PML/RARA mutant fusion protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Feb-1997
C;Accession: I54078
R;Yoshida, H.; Naoe, T.; Fukutani, H.; Kiyoi, H.; Kubo, K.; Ohno, R.
Genes Chromosomes Cancer 12, 37-44, 1995
A;Title: Analysis of the joining sequences of the t(15;17) translocation in
human acute promyelocytic leukemia: sequence non-specific recombination between
the PML and RARA genes within identical short stretches.
A;Reference number: I54078; MUID:95194921; PMID:7534109
A;Accession: I54078
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-18 <RES>
A;Cross-references: GB:S76369; NID:g913695
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: PML/RARA
A;Map position: 15q22/17q12
C;Keywords: fusion protein; leukemia

Query Match 29.0%; Score 18; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 6.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FLPVNV 9
||| |
Db 4 FLPNSN 9

RESULT 43

B24749
neuropeptide B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C;Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine.
A;Reference number: A94074; MUID:86067985; PMID:3865193
A;Accession: B24749
A;Molecule type: protein
A;Residues: 1-8 <YAN>
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide

Query Match 27.4%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| | |
Db 1 FLFQP 5

RESULT 44
D28027
protein P7 - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C;Accession: D28027
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-sequence analysis of proteins electroblotted from two-dimensional gel-separated total extracts.
A;Reference number: A94167
A;Accession: D28027
A;Molecule type: protein
A;Residues: 1-10 <BAU>

Query Match 27.4%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPV 7
|:|:
Db 6 FVPI 9

RESULT 45
S68033
cytochrome P450 1A1 - tilapia (fragment)
C;Species: Oreochromis niloticus x Oreochromis aureus (tilapia)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S68033
R;Ueng, Y.F.; Ueng, T.H.

Arch. Biochem. Biophys. 322, 347-356, 1995

A;Title: Induction and purification of cytochrome P450 1A1 from 3-methylcholanthrene-treated tilapia, *Oreochromis niloticus* x *Oreochromis aureus*.

A;Reference number: S68033; MUID:96032654; PMID:7574707

A;Accession: S68033

A;Molecule type: protein

A;Residues: 1-10 <UEN>

A;Experimental source: liver and gill

Query Match 27.4%; Score 17; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 5.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11

|| : |

Db 2 LPFIGAL 8

RESULT 46

B59146

conotoxin au5b - cone shell (*Conus aulicus*)

C;Species: *Conus aulicus* (court cone)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: B59146

R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty, R.; DelaCruz, R.C.; Nielsen, J.S.; Zhou, L.M.; Bandyopadhyay, P.; Craig, A.G.; Olivera, B.M.

J. Biol. Chem. 274, 30664-30671, 1999

A;Title: The T-superfamily of conotoxins.

A;Reference number: A59147; MUID:99452958; PMID:10521453

A;Accession: B59146

A;Molecule type: protein

A;Residues: 1-11 <WAL>

C;Keywords: amidated carboxyl end; toxin; venom

F;2-9,3-10/Disulfide bonds: #status experimental

F;11/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 27.4%; Score 17; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVV 8

|| |:

Db 1 FCCPVI 6

RESULT 47

I40663

bma protein - *Clostridium cochlearium* (fragment)

C;Species: *Clostridium cochlearium*

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999

C;Accession: I40663; S47465

R;Zelder, O.; Beatrix, B.; Leutbecher, U.; Buckel, W.

Eur. J. Biochem. 226, 577-585, 1994

A;Title: Characterization of the coenzyme-B12-dependent glutamate mutase from *Clostridium cochlearium* produced in *Escherichia coli*.

A;Reference number: I40659; MUID:95094816; PMID:7880251

A;Accession: I40663
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-12 <RES>
A;Cross-references: EMBL:X80997; NID:g530005; PIDN:CAA56924.1; PID:g530010
C;Genetics:
A;Gene: bma

Query Match 27.4%; Score 17; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 6.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNL 11
: :|:||
Db 1 MKIVDVL 7

RESULT 48
S50900
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIc protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50900
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylcarbodiimide during inhibition of energy dissipation.
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50900
A;Molecule type: protein
A;Residues: 1-14 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosystem II; thylakoid

Query Match 27.4%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
|||
Db 2 FLP 4

RESULT 49
S27140
hypothetical protein 1 estrogen receptor 5'-region - human
C;Species: Homo sapiens (man)
C;Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000
C;Accession: S27140
R;Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene.
A;Reference number: S27140; MUID:93075998; PMID:1476547
A;Accession: S27140

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <KEA>
A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202
C;Superfamily: unassigned leader peptides

Query Match 27.4%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
|||
Db 6 FLP 8

RESULT 50
S58862
botulinum neurotoxin type A and B hemagglutinin component II - Clostridium
botulinum (strain NCTC 7272) (fragment)
N;Alternate names: HA-II protein
C;Species: Clostridium botulinum
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 15-Oct-1999
C;Accession: S58862; S58858
R;East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum
neurotoxin complex encoded by Clostridium botulinum types A and B.
A;Reference number: S58855
A;Accession: S58862
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <EAS>
A;Cross-references: EMBL:X79104; NID:g870937; PIDN:CAA55719.1; PID:g870941
A;Experimental source: strain NCTC 7272
A;Accession: S58858
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-14 <EA2>
A;Cross-references: EMBL:X79103; NID:g870932; PIDN:CAA55715.1; PID:g870936
A;Experimental source: strain Eklund 17B
C;Keywords: hemagglutinin; neurotoxin

Query Match 27.4%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
|||
Db 7 FLP 9

Search completed: July 4, 2004, 04:47:16
Job time : 10.2239 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 23.5522 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-4
Perfect score: 62
Sequence: 1 LFFFLLPVVNVL 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	62	100.0	12	14	US-10-281-652-4	Sequence 4, Appli
2	31	50.0	9	14	US-10-119-536A-89	Sequence 89, Appli
3	29	46.8	9	14	US-10-119-536A-182	Sequence 182, App
4	29	46.8	10	12	US-09-935-430-446	Sequence 446, App
5	29	46.8	10	14	US-10-277-292-446	Sequence 446, App
6	29	46.8	10	15	US-10-280-340-446	Sequence 446, App
7	29	46.8	11	10	US-09-309-196-57	Sequence 57, Appli
8	29	46.8	11	10	US-09-201-396-38	Sequence 38, Appli
9	29	46.8	11	10	US-09-953-354-68	Sequence 68, Appli
10	29	46.8	11	12	US-09-747-774A-68	Sequence 68, Appli
11	29	46.8	11	12	US-10-263-341-57	Sequence 57, Appli
12	29	46.8	11	14	US-10-277-607-38	Sequence 38, Appli
13	29	46.8	13	14	US-10-116-252-22	Sequence 22, Appli
14	29	46.8	14	12	US-10-014-340-611	Sequence 611, App
15	29	46.8	14	12	US-10-014-340-612	Sequence 612, App
16	29	46.8	18	14	US-10-084-813-249	Sequence 249, App
17	29	46.8	18	14	US-10-084-813-250	Sequence 250, App
18	28	45.2	9	14	US-10-119-536A-84	Sequence 84, Appli
19	28	45.2	9	14	US-10-119-536A-92	Sequence 92, Appli
20	27	43.5	9	16	US-10-447-161-61	Sequence 61, Appli
21	27	43.5	11	10	US-09-201-396-6	Sequence 6, Appli
22	27	43.5	11	14	US-10-277-607-6	Sequence 6, Appli
23	27	43.5	14	14	US-10-269-171A-6	Sequence 6, Appli
24	27	43.5	15	12	US-10-149-135-1941	Sequence 1941, Ap
25	27	43.5	15	12	US-10-149-135-1950	Sequence 1950, Ap
26	27	43.5	15	12	US-10-149-135-2026	Sequence 2026, Ap
27	27	43.5	15	12	US-10-149-135-2412	Sequence 2412, Ap
28	26	41.9	8	15	US-10-137-867-292	Sequence 292, App
29	26	41.9	9	14	US-10-119-536A-176	Sequence 176, App
30	26	41.9	9	14	US-10-119-536A-190	Sequence 190, App
31	26	41.9	9	15	US-10-057-475B-10903	Sequence 10903, A
32	26	41.9	9	15	US-10-057-475B-10956	Sequence 10956, A
33	26	41.9	9	15	US-10-154-884B-10903	Sequence 10903, A
34	26	41.9	9	15	US-10-154-884B-10956	Sequence 10956, A
35	26	41.9	10	9	US-09-777-710A-7	Sequence 7, Appli
36	26	41.9	10	10	US-09-572-404B-1109	Sequence 1109, Ap
37	26	41.9	10	12	US-09-935-430-427	Sequence 427, App
38	26	41.9	10	12	US-09-935-430-503	Sequence 503, App
39	26	41.9	10	12	US-09-935-430-613	Sequence 613, App
40	26	41.9	10	14	US-10-277-292-427	Sequence 427, App
41	26	41.9	10	14	US-10-277-292-503	Sequence 503, App
42	26	41.9	10	14	US-10-277-292-613	Sequence 613, App
43	26	41.9	10	15	US-10-280-340-427	Sequence 427, App
44	26	41.9	10	15	US-10-280-340-503	Sequence 503, App
45	26	41.9	10	15	US-10-280-340-613	Sequence 613, App
46	26	41.9	14	14	US-10-206-699-37	Sequence 37, Appli
47	26	41.9	15	14	US-10-294-891-11	Sequence 11, Appli
48	26	41.9	16	12	US-10-103-395-15	Sequence 15, Appli
49	26	41.9	17	11	US-09-833-245-570	Sequence 570, App
50	26	41.9	18	14	US-10-084-813-248	Sequence 248, App
51	25	40.3	11	14	US-10-119-528-31	Sequence 31, Appli
52	25	40.3	12	14	US-10-269-171A-5	Sequence 5, Appli
53	25	40.3	12	16	US-10-685-898-27	Sequence 27, Appli
54	25	40.3	13	9	US-09-826-290-122	Sequence 122, App
55	25	40.3	13	16	US-10-264-309-305	Sequence 305, App
56	25	40.3	14	12	US-10-162-134A-6	Sequence 6, Appli

57	25	40.3	14	12	US-10-162-134A-10	Sequence 10, Appl
58	25	40.3	14	14	US-10-261-798-40	Sequence 40, Appl
59	25	40.3	16	10	US-09-880-748-2250	Sequence 2250, Ap
60	25	40.3	16	12	US-10-293-418-2250	Sequence 2250, Ap
61	25	40.3	17	9	US-09-071-838-88	Sequence 88, Appl
62	25	40.3	17	10	US-09-759-130B-354	Sequence 354, App
63	25	40.3	17	14	US-10-189-123-84	Sequence 84, Appl
64	25	40.3	17	14	US-10-213-512-88	Sequence 88, Appl
65	25	40.3	17	14	US-10-188-495-84	Sequence 84, Appl
66	25	40.3	17	16	US-10-741-790-354	Sequence 354, App
67	25	40.3	18	9	US-09-005-243-94	Sequence 94, Appl
68	25	40.3	18	9	US-09-005-243-95	Sequence 95, Appl
69	25	40.3	18	9	US-09-224-683-94	Sequence 94, Appl
70	25	40.3	18	9	US-09-224-683-95	Sequence 95, Appl
71	24	38.7	12	14	US-10-075-869-41	Sequence 41, Appl
72	24	38.7	12	15	US-10-366-493-41	Sequence 41, Appl
73	24	38.7	12	16	US-10-688-100-7	Sequence 7, Appli
74	24	38.7	12	16	US-10-685-898-42	Sequence 42, Appl
75	24	38.7	14	12	US-10-601-837-138	Sequence 138, App
76	24	38.7	14	12	US-10-162-134A-7	Sequence 7, Appli
77	24	38.7	14	14	US-10-281-478-81	Sequence 81, Appl
78	24	38.7	14	15	US-10-394-980-113	Sequence 113, App
79	24	38.7	15	12	US-10-149-135-1959	Sequence 1959, Ap
80	24	38.7	15	14	US-10-213-473-5	Sequence 5, Appli
81	24	38.7	15	14	US-10-132-100-5	Sequence 5, Appli
82	24	38.7	16	10	US-09-880-748-2256	Sequence 2256, Ap
83	24	38.7	16	12	US-10-293-418-2256	Sequence 2256, Ap
84	24	38.7	17	14	US-10-224-999A-1559	Sequence 1559, Ap
85	24	38.7	17	14	US-10-029-386-33351	Sequence 33351, A
86	24	38.7	18	14	US-10-224-999A-1573	Sequence 1573, Ap
87	24	38.7	18	14	US-10-224-999A-1574	Sequence 1574, Ap
88	23	37.1	7	14	US-10-286-457-477	Sequence 477, App
89	23	37.1	7	16	US-10-685-898-11	Sequence 11, Appl
90	23	37.1	8	8	US-08-979-847-150	Sequence 150, App
91	23	37.1	8	8	US-08-979-847-151	Sequence 151, App
92	23	37.1	8	8	US-08-979-847-152	Sequence 152, App
93	23	37.1	8	11	US-09-943-944E-199	Sequence 199, App
94	23	37.1	8	12	US-10-149-135-454	Sequence 454, App
95	23	37.1	8	12	US-10-149-135-747	Sequence 747, App
96	23	37.1	8	12	US-10-149-135-1279	Sequence 1279, Ap
97	23	37.1	8	12	US-10-149-135-1906	Sequence 1906, Ap
98	23	37.1	8	12	US-10-149-135-2251	Sequence 2251, Ap
99	23	37.1	8	14	US-10-114-104-150	Sequence 150, App
100	23	37.1	8	14	US-10-114-104-151	Sequence 151, App

ALIGNMENTS

RESULT 1
 US-10-281-652-4
 ; Sequence 4, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOUGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-4

Query Match 100.0%; Score 62; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF LPV VNV LP 12
||| ||| ||| |||
Db 1 LFFF LPV VNV LP 12

RESULT 2
US-10-119-536A-89
; Sequence 89, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular
Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-89

Query Match 50.0%; Score 31; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFF LPVV 8
|| |||:
Db 2 LFTFLPII 9

RESULT 3

US-10-119-536A-182

; Sequence 182, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide

US-10-119-536A-182

Query Match 46.8%; Score 29; DB 14; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.2e+06;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFF LPVV 8
|| |:::
Db 2 LFTFMPII 9

RESULT 4

US-09-935-430-446

; Sequence 446, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS

; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-446

Query Match 46.8%; Score 29; DB 12; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFFLPVVNVL 11
| ||| |:|
Db 1 FTHLPVSNIL 10

RESULT 5
US-10-277-292-446
; Sequence 446, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-446

Query Match 46.8%; Score 29; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFFLPVVNL 11
| ||| |:
Db 1 FTHLPVSNIL 10

RESULT 6

US-10-280-340-446

; Sequence 446, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-446

Query Match 46.8%; Score 29; DB 15; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FFFLPVVNL 11
| ||| |:
Db 1 FTHLPVSNIL 10

RESULT 7

US-09-309-196-57

; Sequence 57, Application US/09309196
; Publication No. US20030008380A1
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,196
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,137
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLKES=2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-309-196-57

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2' FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 8
US-09-201-396-38
; Sequence 38, Application US/09201396A
; Publication No. US20030009022A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9
; CURRENT APPLICATION NUMBER: US/09/201,396A
; CURRENT FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: 08/582,333
; EARLIER FILING DATE: 1996-01-17
; EARLIER APPLICATION NUMBER: 08/322,137
; EARLIER FILING DATE: 1994-10-13
; EARLIER APPLICATION NUMBER: 08/309,313
; EARLIER FILING DATE: 1994-09-20
; EARLIER APPLICATION NUMBER: 08/190,328
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/041,431
; EARLIER FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-201-396-38

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2' FFFLP 6
|||||
Db 6 FFFLP 10

RESULT 9
US-09-953-354-68
; Sequence 68, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for

Identifying Receptor Effectors
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,354
FILING DATE: 13-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,172
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: CPI-012CP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-953-354-68

Query Match 46.8%; Score 29; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|||
Db 6 FFFLP 10

RESULT 10
US-09-747-774A-68
; Sequence 68, Application US/09747774A
; Publication No. US20010026926A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J. M.
; APPLICANT: Broach, James R.
; APPLICANT: Manfredi, John
; APPLICANT: Paul, Jeremy
; APPLICANT: Fowlkes, Dana M.

; APPLICANT: Trueheart, Joshua
; TITLE OF INVENTION: Methods and Compositions for Identifying
; TITLE OF INVENTION: Receptor Effectors
; FILE REFERENCE: CPI-012CP5DV
; CURRENT APPLICATION NUMBER: US/09/747,774A
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 08/582,333
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: US 08/464,531
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/461,598
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/461,383
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/463,181
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/322,137
; PRIOR FILING DATE: 1994-10-13
; PRIOR APPLICATION NUMBER: US 08/309,313
; PRIOR FILING DATE: 1994-09-20
; PRIOR APPLICATION NUMBER: US 08/190,328
; PRIOR FILING DATE: 1994-01-31
; PRIOR APPLICATION NUMBER: US 08/041,431
; PRIOR FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
US-09-747-774A-68

Query Match 46.8%; Score 29; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| || ||
Db 6 FFFLP 10

RESULT 11
US-10-263-341-57
; Sequence 57, Application US/10263341
; Publication No. US20030203417A1
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; BROACH, Jim
; MANFREDI, John
; KLEIN, Christine
; MURPHY, Andrew J.
; PAUL, Jeremy
; TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; PHERMONE SYSTEM PROTEIN SURROGATES, AND USES
THEREFOR
; NUMBER OF SEQUENCES: 119

;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: BROWDY AND NEIMARK
;
; STREET: 419 Seventh Street, N.W., Suite 300
;
; CITY: Washington
;
; STATE: D.C.
;
; COUNTRY: USA
;
; ZIP: 20004
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/10/263,341
;
; FILING DATE: 01-Oct-2002
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/322,137
;
; FILING DATE: 13-OCT-1994
;
; APPLICATION NUMBER: US 08/309,313
;
; FILING DATE: 20-SEP-1994
;
; APPLICATION NUMBER: US 08/190,328
;
; FILING DATE: 31-JAN-1994
;
; APPLICATION NUMBER: US 08/041,431
;
; FILING DATE: 31-MAR-1993
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: COOPER, Iver P.
;
; REGISTRATION NUMBER: 28,005
;
; REFERENCE/DOCKET NUMBER: FOLWES=2C
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 202-628-5197
;
; TELEFAX: 202-737-3528
;
; TELEX: 248633
;
; INFORMATION FOR SEQ ID NO: 57:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 11 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-263-341-57

Query Match 46.8%; Score 29; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
 |||||
Db 6 FFFLP 10

RESULT 12
US-10-277-607-38
;
; Sequence 38, Application US/10277607
;
; Publication No. US20030166143A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Klein, Christine A.

; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy I.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9CN
; CURRENT APPLICATION NUMBER: US/10/277,607
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 09/201,396
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 60/109,902
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US98/21168
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 08/946,298
; PRIOR FILING DATE: 1997-10-07
; PRIOR APPLICATION NUMBER: 08/689,172
; PRIOR FILING DATE: 1996-08-06
; PRIOR APPLICATION NUMBER: 08/582,333
; PRIOR FILING DATE: 1996-01-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-10-277-607-38

Query Match 46.8%; Score 29; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
 |||||
Db 6 FFFLP 10

RESULT 13
US-10-116-252-22
; Sequence 22, Application US/10116252
; Publication No. US20030028008A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,
; TITLE OF INVENTION: Polypeptides, and Antibodies
; FILE REFERENCE: PT007P1
; CURRENT APPLICATION NUMBER: US/10/116,252
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US/09/711,909
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: PCT/US00/13737
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/135,167
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/143,616

; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 60/152,934
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/189,029
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-252-22

Query Match 46.8%; Score 29; DB 14; Length 13;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFPLPVNVNL 11
| ||||: :|
Db 2 LEFFLPLALIL 12

RESULT 14

US-10-014-340-611
; Sequence 611, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 611
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-611

Query Match 46.8%; Score 29; DB 12; Length 14;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PVVNVL 12
| :|||
Db 4 PPINVLP 10

RESULT 15

US-10-014-340-612
; Sequence 612, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor,
Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 612
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-612

Query Match 46.8%; Score 29; DB 12; Length 14;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 6 PVVNVL 12
| :|||
Db 4 PPINVLP 10

RESULT 16
US-10-084-813-249
; Sequence 249, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-249

Query Match 46.8%; Score 29; DB 14; Length 18;
Best Local Similarity 45.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LFFFPLPVVNVL 11
| |||||:: ::
Db 6 LGFFPLLLTMI 16

RESULT 17
US-10-084-813-250
; Sequence 250, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-250

Query Match 46.8%; Score 29; DB 14; Length 18;
Best Local Similarity 45.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFPLPVVNVL 11
| ||||:: ::
Db 2 LGFFPLPLLTMI 12

RESULT 18
US-10-119-536A-84
; Sequence 84, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular
Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)

; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-84

Query Match 45.2%; Score 28; DB 14; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVVNV 10
| |||:: |
Db 1 FTFLPIILV 9

RESULT 19

US-10-119-536A-92

; Sequence 92, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-92

Query Match 45.2%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNL 11
| |||:: ||
Db 1 FLPIILVL 8

RESULT 20

US-10-447-161-61

; Sequence 61, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-61

Query Match 43.5%; Score 27; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFPLP 6
::|||
Db 1 VYFFLP 6

RESULT 21
US-09-201-396-6
; Sequence 6, Application US/09201396A
; Publication No. US20030009022A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9
; CURRENT APPLICATION NUMBER: US/09/201,396A
; CURRENT FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: 08/582,333
; EARLIER FILING DATE: 1996-01-17
; EARLIER APPLICATION NUMBER: 08/322,137
; EARLIER FILING DATE: 1994-10-13
; EARLIER APPLICATION NUMBER: 08/309,313
; EARLIER FILING DATE: 1994-09-20
; EARLIER APPLICATION NUMBER: 08/190,328
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/041,431
; EARLIER FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-201-396-6

Query Match 43.5%; Score 27; DB 10; Length 11;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 FFFLPV 7
||| ||
Db 3 FFFRPV 8

RESULT 22

US-10-277-607-6

; Sequence 6, Application US/10277607
; Publication No. US20030166143A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy I.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9CN
; CURRENT APPLICATION NUMBER: US/10/277,607
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 09/201,396
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: 60/109,902
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US98/21168
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 08/946,298
; PRIOR FILING DATE: 1997-10-07
; PRIOR APPLICATION NUMBER: 08/689,172
; PRIOR FILING DATE: 1996-08-06
; PRIOR APPLICATION NUMBER: 08/582,333
; PRIOR FILING DATE: 1996-01-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct

US-10-277-607-6

Query Match 43.5%; Score 27; DB 14; Length 11;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 FFFLPV 7
||| ||
Db 3 FFFRPV 8

RESULT 23

US-10-269-171A-6

; Sequence 6, Application US/10269171A
; Publication No. US20030095979A1
; GENERAL INFORMATION:

; APPLICANT: Frank Mattner
; APPLICANT: Wolfgang Zauner
; APPLICANT: Walter Schmidt
; APPLICANT: Michael Buschle
; TITLE OF INVENTION: Pharmaceutical preparations comprising modified
; TITLE OF INVENTION: peptides
; FILE REFERENCE: SONN:020US
; CURRENT APPLICATION NUMBER: US/10/269,171A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/EPO1/04313
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-269-171A-6

Query Match 43.5%; Score 27; DB 14; Length 14;
Best Local Similarity 33.3%; Pred. No. 7.1e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFLLPVVN 9
:| |: ::|
Db 2 IFIFISIIN 10

RESULT 24
US-10-149-135-1941
; Sequence 1941, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29

; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1941
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1941

Query Match 43.5%; Score 27; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFLLPVVNVL P 12
| | : || |:|
Db 3 LVFGIEVVEVVP 14

RESULT 25

US-10-149-135-1950

; Sequence 1950, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1950

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1950

Query Match 43.5%; Score 27; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVNVLP 12
| | : || |:
Db 2 LVFGIEVVEVVP 13

RESULT 26

US-10-149-135-2026

; Sequence 2026, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2026

Query Match 43.5%; Score 27; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVNVLP 12
| | : || |:|
Db 2 LVFGIEVVEVVP 13

RESULT 27

US-10-149-135-2412

; Sequence 2412, Application US/10149135

; Publication No. US20040053822A1

; GENERAL INFORMATION:

; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa

; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0130001

; CURRENT APPLICATION NUMBER: US/10/149,135

; CURRENT FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: PCT/US00/33545

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/458,298

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 09/189,702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/205,713

; PRIOR FILING DATE: 1994-03-04

; PRIOR APPLICATION NUMBER: US 08/159,184

; PRIOR FILING DATE: 1993-11-29

; PRIOR APPLICATION NUMBER: US 08/073,205

; PRIOR FILING DATE: 1993-06-04

; PRIOR APPLICATION NUMBER: US 08/027,146

; PRIOR FILING DATE: 1993-03-05

; NUMBER OF SEQ ID NOS: 2479

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2412

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial Peptide

US-10-149-135-2412

Query Match 43.5%; Score 27; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LFFFPLPVNVLP 12
| | : || |:|
Db 2 LVFGIEVVEVVP 13

RESULT 28

US-10-137-867-292

; Sequence 292, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 292
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-137-867-292

Query Match 41.9%; Score 26; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 5

|||||

Db 1 LFFF 5

RESULT 29

US-10-119-536A-176

; Sequence 176, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular
Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A

; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)<223> CT841 immunogenic peptide
US-10-119-536A-176

Query Match 41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVVNV 10
| :|:: |
Db 1 FTFMPIILV 9

RESULT 30
US-10-119-536A-190
; Sequence 190, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CT841 immunogenic peptide
US-10-119-536A-190

Query Match 41.9%; Score 26; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNL 11
| :|:: ||
Db 1 FMPIILV 8

RESULT 31

US-10-057-475B-10903

; Sequence 10903, Application US/10057475B

; Publication No. US20040002068A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algat, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Clapper, Jonathan David

; APPLICANT: Wang, Aijun

; APPLICANT: Ordonez, Nadia

; APPLICANT: Carter, Lauren

; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-014402US

; CURRENT APPLICATION NUMBER: US/10/057,475B

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 10903

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Ly1484 long MHC HLA A24 class I binding peptide

US-10-057-475B-10903

Query Match 41.9%; Score 26; DB 15; Length 9;

Best Local Similarity 80.0%; Pred. No. 1.2e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6

||:||
Db 2 FFYLP 6

RESULT 32
US-10-057-475B-10956
; Sequence 10956, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10956
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A24 class I binding peptide
US-10-057-475B-10956

Query Match 41.9%; Score 26; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
||:||
Db 2 FFYLP 6

RESULT 33
US-10-154-884B-10903
; Sequence 10903, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10903
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 long MHC HLA A24 class I binding peptide
US-10-154-884B-10903

Query Match 41.9%; Score 26; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
||:||
Db 2 FFYLP 6

RESULT 34
US-10-154-884B-10956
; Sequence 10956, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10956
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A24 class I binding peptide
US-10-154-884B-10956

Query Match 41.9%; Score 26; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFLP 6
 ||:||
Db 2 FFYLP 6

RESULT 35
US-09-777-710A-7
; Sequence 7, Application US/09777710A
; Patent No. US20020058305A1
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. US20020058305A1omu et al.
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-7

Query Match 41.9%; Score 26; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNV 10
 || |||:
Db 2 FLEVVNI 8

RESULT 36
US-09-572-404B-1109
; Sequence 1109, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1109
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in BONZO OR STRL33 OR TYMSTR at 197-206
and may
; OTHER INFORMATION: interact with Sequence 1110 in this patent.
US-09-572-404B-1109

Query Match 41.9%; Score 26; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFF LPVV 8
| ||| |:::
Db 2 LGFF LPPLL 9

RESULT 37

US-09-935-430-427

; Sequence 427, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 427
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-935-430-427

Query Match 41.9%; Score 26; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNVL 11
| | | |:::
Db 1 LPVSNIL 7

RESULT 38

US-09-935-430-503

; Sequence 503, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-503

Query Match 41.9%; Score 26; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11
||| :|
Db 1 LPVSNIL 7

RESULT 39
US-09-935-430-613
; Sequence 613, Application US/09935430
; Publication No. US20030017466A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/09/935,430
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 613
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-935-430-613

Query Match 41.9%; Score 26; DB 12; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNL 11
||| :|
Db 1 LPVSNIL 7

RESULT 40

US-10-277-292-427

; Sequence 427, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 427
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-427

Query Match 41.9%; Score 26; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNL 11
||| :|
Db 1 LPVSNIL 7

RESULT 41
US-10-277-292-503
; Sequence 503, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-503

Query Match 41.9%; Score 26; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNVNL 11
 ||| :|
Db 1 LPVSNIL 7

RESULT 42
US-10-277-292-613
; Sequence 613, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 613
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-613

Query Match 41.9%; Score 26; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNVL 11
 ||| :|
Db 1 LPVSNIL 7

RESULT 43
US-10-280-340-427
; Sequence 427, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 427

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-427

Query Match 41.9%; Score 26; DB 15; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNVNL 11
||| :|:
Db 1 LPVSNIL 7

RESULT 44
US-10-280-340-503

; Sequence 503, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-503

Query Match 41.9%; Score 26; DB 15; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNVNL 11
||| :|:
Db 1 LPVSNIL 7

RESULT 45
US-10-280-340-613
; Sequence 613, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280, 340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935, 430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227, 098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282, 739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 613
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-613

Query Match 41.9%; Score 26; DB 15; Length 10;
Best Local Similarity 71.4%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNVNL 11
||| :|
Db 1 LPVSNIL 7

RESULT 46
US-10-206-699-37
; Sequence 37, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206, 699
; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-37

Query Match 41.9%; Score 26; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVNVNLP 12
||| : ||
Db 3 LPVFSTLP 10

RESULT 47

US-10-294-891-11

; Sequence 11, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-11

Query Match 41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFFLPVVNVL 11
|:|| :| ::
Db 2 FYFLILVRII 11

RESULT 48

US-10-103-395-15
; Sequence 15, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-15

Query Match 41.9%; Score 26; DB 12; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVVNV 10
 |||| : |
Db 5 FFLPALPV 12

RESULT 49
US-09-833-245-570
; Sequence 570, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 570

; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-570

Query Match 41.9%; Score 26; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFFL 5
| |||||
Db 5 LFFFL 9

RESULT 50

US-10-084-813-248

; Sequence 248, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-248

Query Match 41.9%; Score 26; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFFLPVV 8
| ||||:|:
Db 10 LGFFLPPLL 17

Search completed: July 4, 2004, 05:12:26
Job time : 25.5522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:51 ; Search time 20.4179 Seconds
(without alignments)
185.436 Million cell updates/sec

Title: US-09-641-802-4

Perfect score: 62

Sequence: 1 LFFFLLPVVVNVLP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

Description

1	26	41.9	12	13	P82820	P82820 rana catesb
2	26	41.9	13	13	P82848	P82848 rana pipien
3	26	41.9	17	8	Q8HKE6	Q8hke6 rhipicephal
4	26	41.9	17	11	Q9ERZ2	Q9erz2 mus musculu
5	25	40.3	15	7	Q9TNQ1	Q9tnq1 mus sp. bet
6	24	38.7	18	11	Q7TQB5	Q7tqb5 mus musculu
7	24	38.7	18	12	Q9IBM7	Q9ibm7 autographa
8	23	37.1	17	8	Q8HKF6	Q8hkf6 rhipicephal
9	23	37.1	18	4	Q8NED1	Q8ned1 homo sapien
10	22	35.5	15	2	Q46456	Q46456 clostridium
11	22	35.5	15	8	Q36727	Q36727 homo sapien
12	22	35.5	17	6	Q95KQ7	Q95kq7 sus scrofa
13	22	35.5	17	11	Q80T36	Q80t36 mus musculu
14	21.5	34.7	14	13	P82832	P82832 rana luteiv
15	21	33.9	9	3	Q9P8E5	Q9p8e5 kluyveromyc
16	21	33.9	11	6	Q9TQS0	Q9tqs0 bos taurus
17	21	33.9	15	11	Q9QVD7	Q9qvd7 rattus sp.
18	21	33.9	17	3	Q9URC6	Q9urc6 saccharomyc
19	21	33.9	17	4	O95795	O95795 homo sapien
20	21	33.9	17	8	Q95F78	Q95f78 hizikia fus
21	21	33.9	18	8	O19979	O19979 gossypium d
22	21	33.9	18	8	O19969	O19969 gossypium a
23	20	32.3	8	10	Q40530	Q40530 nicotiana t
24	20	32.3	10	13	Q7ZZI2	Q7zzi2 salvelinus
25	20	32.3	14	2	P81715	P81715 streptomyce
26	20	32.3	14	8	Q8M099	Q8m099 tockus nasu
27	20	32.3	14	10	P82340	P82340 pisum sativ
28	20	32.3	15	2	O68425	O68425 buchnera ap
29	20	32.3	15	16	Q8XF44	Q8xf44 salmonella
30	20	32.3	16	1	Q9UWK4	Q9uwk4 methanobact
31	20	32.3	17	3	Q06800	Q06800 saccharomyc
32	20	32.3	18	8	Q8M0A0	Q8m0a0 tockus leuc
33	19	30.6	8	2	P83532	P83532 lactobacill
34	19	30.6	9	8	Q9GD36	Q9gd36 juncus effu
35	19	30.6	11	2	Q9AIZ7	Q9aiz7 carsonella
36	19	30.6	12	8	Q9GI96	Q9gi96 sargassum p
37	19	30.6	12	8	Q37071	Q37071 petunia hyb
38	19	30.6	13	4	Q14462	Q14462 homo sapien
39	19	30.6	13	4	Q16007	Q16007 homo sapien
40	19	30.6	13	11	Q9QVK6	Q9qvk6 rattus sp.
41	19	30.6	13	12	Q9PXB5	Q9pxb5 duck hepati
42	19	30.6	13	13	P82884	P82884 rana clamit
43	19	30.6	14	5	Q26100	Q26100 pratylenchu
44	19	30.6	15	5	Q9TWF5	Q9twf5 artemia (br
45	19	30.6	15	10	Q9S8F1	Q9s8f1 zea mays (m
46	19	30.6	16	2	O30985	O30985 rhodobacter
47	19	30.6	16	2	Q8VNS8	Q8vns8 escherichia
48	19	30.6	16	3	O94554	O94554 schizosacch
49	19	30.6	16	5	Q26101	Q26101 pratylenchu
50	19	30.6	16	8	O19977	O19977 gossypium m
51	19	30.6	16	8	O19975	O19975 gossypium t
52	19	30.6	16	8	O19973	O19973 gossypium b
53	19	30.6	16	8	O19971	O19971 gossypium h
54	19	30.6	16	16	Q8D183	Q8d183 yersinia pe
55	19	30.6	17	4	Q9UCP4	Q9ucp4 homo sapien
56	19	30.6	17	4	Q9HBD8	Q9hbd8 homo sapien
57	19	30.6	17	8	Q8HKJ4	Q8hkj4 amblyomma h

58	19	30.6	17	8	Q8HKI8	Q8hki8 amblyomma v
59	19	30.6	17	8	Q8HKH3	Q8hkh3 boophilus a
60	19	30.6	18	5	Q9TWE0	Q9twe0 biomphalari
61	19	30.6	18	8	Q8HSM0	Q8hsm0 spyridia fi
62	18.5	29.8	17	12	Q65373	Q65373 orgyia pseu
63	18	29.0	8	2	Q8GMM5	Q8gmm5 acinetobact
64	18	29.0	8	2	Q849P4	Q849p4 salmonella
65	18	29.0	9	2	P82568	P82568 streptococc
66	18	29.0	9	8	Q9TJ87	Q9tj87 caloglossa
67	18	29.0	9	8	Q8W7T9	Q8w7t9 bostrychia
68	18	29.0	9	8	Q9T389	Q9t389 caloglossa
69	18	29.0	9	8	O78337	O78337 caloglossa
70	18	29.0	9	8	Q9T388	Q9t388 caloglossa
71	18	29.0	9	8	Q8ME58	Q8me58 porphyra li
72	18	29.0	9	8	Q9TJ85	Q9tj85 caloglossa
73	18	29.0	9	8	Q95BY3	Q95by3 caloglossa
74	18	29.0	9	8	Q9MVU2	Q9mvu2 caloglossa
75	18	29.0	9	8	Q8MDU2	Q8mdu2 hypnea sp.
76	18	29.0	9	8	Q8ME56	Q8me56 porphyra mi
77	18	29.0	9	8	Q8HSL5	Q8hsl5 spyridia fi
78	18	29.0	9	8	Q8HSL0	Q8hsl0 murrayella
79	18	29.0	9	8	Q8HRK0	Q8hrk0 gracilaria
80	18	29.0	9	8	Q8HRJ8	Q8hrj8 ptilophora
81	18	29.0	9	8	Q8HB45	Q8hb45 gracilaria
82	18	29.0	9	8	Q8HB44	Q8hb44 gracilaria
83	18	29.0	9	8	Q8HB43	Q8hb43 gracilaria
84	18	29.0	9	8	Q9TLD0	Q9tld0 bostrychia
85	18	29.0	9	8	Q9T387	Q9t387 bostrychia
86	18	29.0	9	10	O81966	O81966 caloglossa
87	18	29.0	9	10	O81964	O81964 caloglossa
88	18	29.0	9	10	O81962	O81962 caloglossa
89	18	29.0	9	10	O82778	O82778 caloglossa
90	18	29.0	9	10	O81968	O81968 caloglossa
91	18	29.0	10	8	Q8WBR7	Q8wbr7 chaitophoru
92	18	29.0	10	8	Q8ME52	Q8me52 porphyra pu
93	18	29.0	10	8	Q9TLC8	Q9tlc8 bostrychia
94	18	29.0	11	4	Q8IVG8	Q8ivg8 homo sapien
95	18	29.0	11	7	Q9TQB3	Q9tqb3 homo sapien
96	18	29.0	11	7	O77874	O77874 oreochromis
97	18	29.0	11	7	O77875	O77875 oreochromis
98	18	29.0	11	8	Q8ME54	Q8me54 porphyra um
99	18	29.0	11	12	Q80GPO	Q80gp0 tomato leaf
100	18	29.0	12	10	P82441	P82441 nicotiana t

ALIGNMENTS

RESULT 1

P82820

ID P82820 PRELIMINARY; PRT; 12 AA.

AC P82820;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE RANATUERIN 5.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranatuerins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, *Rana catesbeiana*.";
RL Biochem. Biophys. Res. Commun. 250:589-592(1998).
CC --!- SUBCELLULAR LOCATION: SECRETED.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;

Query Match 41.9%; Score 26; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNVL 11
|||: ::|
Db 1 FLPIASLL 8

RESULT 2
P82848
ID P82848 PRELIMINARY; PRT; 13 AA.
AC P82848;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Temporin-1P.
OS *Rana pipiens* (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs *Rana luteiventris*,
RT *Rana berlandieri* and *Rana pipiens*.";
RL Eur. J. Biochem. 267:894-900(2000).
CC --!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC --!- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.
CC --!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
DR GO; GO:0006805; P:xenobiotic metabolism; IEA.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1370 MW; 3EF3402B9DF92338 CRC64;

Query Match 41.9%; Score 26; DB 13; Length 13;
Best Local Similarity 62.5%; Pred. No. 9.4e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 4 FLPVVNVL 11
|||:| |
Db 1 FLPIVGKL 8

RESULT 3

Q8HKE6
ID Q8HKE6 PRELIMINARY; PRT; 17 AA.
AC Q8HKE6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Rhipicephalus pulchellus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=72859;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell N.J.H., Murrell A., Barker S.C.;
RT "The value of idiosyncratic markers and conserved tRNA sequences from
RT the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for
RT phylogenetic inference.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY059228; AAL79425.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2121 MW; 15A93BBC1743136 CRC64;

Query Match 41.9%; Score 26; DB 8; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 2 FFFLPVVNVL 11
| || ::| :
Db 2 FMFLSMINFI 11

RESULT 4

Q9ERZ2
ID Q9ERZ2 PRELIMINARY; PRT; 17 AA.
AC Q9ERZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Protein tyrosine phosphatase RPTP-GMC1 (Fragment).
GN PTPRQ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Wright M.B., Foernzler D., Pech M.;
 RT "Organization of the mouse Ptprr gene encoding protein-tyrosine
 phosphatase rPTP-GMC1.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF265561; AAG22700.1; -.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2001 MW; 834A1F2920F07DBF CRC64;

 Query Match 41.9%; Score 26; DB 11; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LFFF 5
 |||||
 Db 4 LFFF 8

 RESULT 5
 Q9TNQ1
 ID Q9TNQ1 PRELIMINARY; PRT; 15 AA.
 AC Q9TNQ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Beta 2M- class I-binding PEPTIDE=MAJOR histocompatibility complex
 DE H-2KB-specific molecule POORLY associated with beta 2-microglobulin
 DE (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94240094; PubMed=8183884;
 RA Joyce S., Kuzushima K., Kepecs G., Angeletti R.H., Nathenson S.G.;
 RT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2Kb) associated with unusually
 RT long peptides: implications for antigen processing and presentation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

 Query Match 40.3%; Score 25; DB 7; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 5 LPVVNL 11
 |||| |:
 Db 7 LPVVKVM 13

 RESULT 6
 Q7TQB5

ID Q7TQB5 PRELIMINARY; PRT; 18 AA.
AC Q7TQB5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Programmed cell death 1 ligand 2 (Fragment).
GN PDCD1LG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gorski K.S., Tsuchiya H., Pardoll D.M.;
RT "A Set of Genes Selectively Expressed in Murine Dendritic Cells:
RT Utility of Related Cis-acting Sequences for Lentiviral Gene
RT Transfer.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY225192; AAO34707.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1999 MW; A9B68E778F78F517 CRC64;

Query Match 38.7%; Score 24; DB 11; Length 18;
Best Local Similarity 30.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFLLPVVNV 10
: ||::|:
Db 1 MLLLLPILNL 10

RESULT 7
Q9IBM7
ID Q9IBM7 PRELIMINARY; PRT; 18 AA.
AC Q9IBM7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE P10 peptide (Fragment).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90085829; PubMed=2688302;
RA Kuzio J., Jaques R., Faulkner P.;
RT "Identification of p74, a gene essential for virulence of baculovirus
RT occlusion bodies.";
RL Virology 173:759-763(1989).
DR EMBL; M31301; AAA46728.2; -.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 1923 MW; FAA5B122C2BFD17A CRC64;

Query Match 38.7%; Score 24; DB 12; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVVNVLP 12
| ||| :|
Db 9 LVVVNAVP 16

RESULT 8
Q8HKE6
ID Q8HKE6 PRELIMINARY; PRT; 17 AA.
AC Q8HKE6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Rhipicephalus evertsi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
OX NCBI_TaxID=60190;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell N.J.H., Murrell A., Barker S.C.;
RT "The value of idiosyncratic markers and conserved tRNA sequences from
RT the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for
RT phylogenetic inference.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY059219; AAL79415.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2071 MW; 15AFFD0CC1743422 CRC64;

Query Match 37.1%; Score 23; DB 8; Length 17;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 FFFLPVVNL 11
| ||| | | :
Db 2 FIFLSVNNFI 11

RESULT 9
Q8NED1
ID Q8NED1 PRELIMINARY; PRT; 18 AA.
AC Q8NED1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;

RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC032027; AAH32027.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 2050 MW; E71A655E65FD253F CRC64;

Query Match 37.1%; Score 23; DB 4; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6
|| ||
Db 1 FFLLP 5

RESULT 10
Q46456
ID Q46456 PRELIMINARY; PRT; 15 AA.
AC Q46456;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Tetanus toxin (Fragment).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053814; PubMed=3536478;
RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J., Weller U.,
RA Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in *E. coli*, and homology
RT with botulinum toxins.";
RL EMBO J. 5:2495-2502(1986).
DR EMBL; X04436; CAA28032.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1706 MW; 08110F73DCCD7EC5 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PVVNVL 11
|:|| |
Db 7 PIVNKL 12

RESULT 11
Q36727
ID Q36727 PRELIMINARY; PRT; 15 AA.
AC Q36727;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ND2 protein (Fragment).

GN ND2.
 OS Homo sapiens (Human).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94380052; PubMed=8093052;
 RA Kosel S., Egensperger R., Mehraein P., Graeber M.B.;
 RT "No association of mutations at nucleotide 5460 of mitochondrial NADH
 dehydrogenase with Alzheimer's disease.";
 RL Biochem. Biophys. Res. Commun. 203:745-749(1994).
 DR EMBL; S73804; AAD14133.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1923 MW; D58870FF163B6060 CRC64;

 Query Match 35.5%; Score 22; DB 8; Length 15;
 Best Local Similarity 37.5%; Pred. No. 5.3e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 LFFF LPVV 8
 | : | : | ::
 Db 6 LYFY LRLI 13

 RESULT 12
 Q95KQ7
 ID Q95KQ7 PRELIMINARY; PRT; 17 AA.
 AC Q95KQ7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE B-cell CLL/lymphoma 9 (Fragment).
 GN BCL9.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knoll A., Dvorak J., Rohrer G., Cepica S.;
 RT "Linkage and cytogenetic mapping of the BCL9 gene to porcine
 chromosome 4.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ416470; CAC94923.1; -.
 KW B-cell.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1825 MW; 90F402DC8CC5F231 CRC64;

 Query Match 35.5%; Score 22; DB 6; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LPVVNVLP 12
|| :| :|
Db 10 LPSMNNMP 17

RESULT 13

Q80T36

ID Q80T36 PRELIMINARY; PRT; 17 AA.
AC Q80T36;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G protein-coupled receptor brain-specific angiogenesis inhibitor 1
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22584407; PubMed=12679517;
RA Vassilatis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
RA Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
RA Bergmann J.E., Gaitanaris G.A.;
RT "The G Protein-Coupled Receptor Repertoires of Human and Mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).
DR EMBL; AY255613; AAO85125.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2133 MW; A20F02808DBA5BFB CRC64;

Query Match 35.5%; Score 22; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FFFL 5
||||
Db 3 FFFL 6

RESULT 14

P82832

ID P82832 PRELIMINARY; PRT; 14 AA.
AC P82832;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Temporin-1LC.
OS Rana luteiventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=58176;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;

RX MEDLINE=20117700; PubMed=10651828;
 RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
 RA Conlon J.M.;
 RT "Peptides with antimicrobial activity from four different families
 RT isolated from the skins of the North American frogs *Rana luteiventris*,
 RT *Rana berlandieri* and *Rana pipiens*.";
 RL Eur. J. Biochem. 267:894-900(2000).
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
 CC S.AUREUS. WEAK ACTIVITY AGAINST GRAM-NEGATIVE BACTERIUM E.COLI AND
 CC THE YEAST C.ALBICANS.
 CC -!- MASS SPECTROMETRY: MW=1603.1; METHOD=ELECTROSPRAY.
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 DR GO; GO:0003799; F:antifungal peptide activity; IEA.
 DR GO; GO:0006805; P:xenobiotic metabolism; IEA.
 KW Antibiotic; Amidation; Fungicide.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;

 Query Match 34.7%; Score 21.5; DB 13; Length 14;
 Best Local Similarity 44.4%; Pred. No. 6.1e+03;
 Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

 Qy 4 FLPV-VNVL 11
 |||: :|:
 Db 1 FLPILINLI 9

RESULT 15
 Q9P8E5
 ID Q9P8E5 PRELIMINARY; PRT; 9 AA.
 AC Q9P8E5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE HIS4 protein (Fragment).
 GN HIS4.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL-Y1140;
 RX MEDLINE=99448382; PubMed=10518937;
 RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
 RT "Kluyveromyces lacxtis HIS4 transcriptional regulation: similarities
 RT and differences to *Saccharomyces cerevisiae* HIS4 gene.";
 RL FEBS Lett. 458:72-76(1999).
 DR EMBL; AJ238494; CAB87125.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

 Query Match 33.9%; Score 21; DB 3; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
| | | | |
Db 2 LPVVNV 7

RESULT 16

Q9TQS0

ID Q9TQS0 PRELIMINARY; PRT; 11 AA.
AC Q9TQS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ243424; CAB60775.1; -.
DR EMBL; AJ243060; CAB60774.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 33.9%; Score 21; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
:|:|:|:
Db 4 VPVVSV 9

RESULT 17

Q9QVD7

ID Q9QVD7 PRELIMINARY; PRT; 15 AA.
AC Q9QVD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inositol 1,4,5-trisphosphate binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain

RT cytosol.";
RL J. Biol. Chem. 267:6518-6525 (1992).
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1726 MW; 1F161D1E2ADF8E8D CRC64;

Query Match 33.9%; Score 21; DB 11; Length 15;
Best Local Similarity 10.0%; Pred. No. 8e+03;
Matches 1; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFFILPVNV 10
: :|: :::::
Db 1 IVYFMAIID 10

RESULT 18
Q9URC6
ID Q9URC6 PRELIMINARY; PRT; 17 AA.
AC Q9URC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipid-binding protein (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91353077; PubMed=1882548;
RA Creutz C.E., Snyder S.L., Kambouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding
proteins of Saccharomyces cerevisiae.";
RL Yeast 7:229-244(1991).
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1959 MW; C2EB6543287744D2 CRC64;

Query Match 33.9%; Score 21; DB 3; Length 17;
Best Local Similarity 33.3%; Pred. No. 8.9e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FLPVVNVLP 12
: :| :| |
Db 4 YVPAFDVAP 12

RESULT 19
O95795
ID O95795 PRELIMINARY; PRT; 17 AA.
AC O95795;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Advanced glycosylation end product-specific receptor (Fragment).
GN RAGE.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blazkova M., Kankova K.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF065211; AAD15888.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 FT VARIANT 9 9 S -> G.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1727 MW; 38C7EE8959E00D72 CRC64;

 Query Match 33.9%; Score 21; DB 4; Length 17;
 Best Local Similarity 80.0%; Pred. No. 8.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 4 FLPVV 8
 ||| |
 Db 12 FLPAV 16

RESULT 20
 Q95F78
 ID Q95F78 PRELIMINARY; PRT; 17 AA.
 AC Q95F78;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase small subunit (Fragment).
 GN RBCS.
 OS Hizikia fusiformis.
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
 OC Hizikia.
 OX NCBI_TaxID=74103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=nep101;
 RA Phillips N.E., Smith C.M., Morden C.W.;
 RT "Testing the systematics of Sargassum (Fucales, Phaeophyceae) with the
 RT Rubisco operon.";
 RL J. Phycol. 0:0-0(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=nep101;
 RA Phillips N.E.;
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
 RT (Fucales, Phaeophyceae).";
 RL Thesis (1998), University of Hawaii.
 DR EMBL; AF292071; AAK83119.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009573; C:ribulose bisphosphate carboxylase complex; IEA.
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
 DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.

DR InterPro; IPR000894; RuBisCO_small.
DR Pfam; PF00101; RuBisCO_small; 1.
KW Chloroplast.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1959 MW; 70C2096FF5A23D12 CRC64;

Query Match 33.9%; Score 21; DB 8; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLP 6
| |||
Db 8 FSFLP 12

RESULT 21
O19979
ID O19979 PRELIMINARY; PRT; 18 AA.
AC O19979;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAI.
OS Gossypium darwinii (Darwin's cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031585; AAC63568.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEFB57 CRC64;

Query Match 33.9%; Score 21; DB 8; Length 18;
Best Local Similarity 37.5%; Pred. No. 9.4e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNL 11
|:|:| ::
Db 11 FVPLVGLV 18

RESULT 22
O19969
ID O19969 PRELIMINARY; PRT; 18 AA.
AC O19969;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAI.
OS Gossypium arboreum (Tree cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031580; AAC63558.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast..
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1942 MW; AC14C3145FAEFB57 CRC64;

Query Match 33.9%; Score 21; DB 8; Length 18;
Best Local Similarity 37.5%; Pred. No. 9.4e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVVNVL 11
|:|:| ::
Db 11 FVPLVGLV 18

RESULT 23
Q40530
ID Q40530 PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE P20 n with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -.
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C9C6 CRC64;

Query Match 32.3%; Score 20; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFFF 4
:|||
Db 1 MFFF 4

RESULT 24

Q7ZZI2
ID Q7ZZI2 PRELIMINARY; PRT; 10 AA.
AC Q7ZZI2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone 2 (Fragment).
OS Salvelinus alpinus (Arctic char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8036;
RN [1]
RP SEQUENCE FROM N.A.
RA McGowan C., Davidson E.A., Davidson W.S.;
RT "Discovering single nucleotide polymorphisms in the introns of fish
RT genes.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY262760; AAP31126.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1134 MW; D0135F972729D2D6 CRC64;

Query Match 32.3%; Score 20; DB 13; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LFFF LPV 7
:| :|||
Db 4 VFLLMPV 10

RESULT 25

P81715
ID P81715 PRELIMINARY; PRT; 14 AA.
AC P81715;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RX PubMed=9531495;
RA Kim I.S., Kim Y.B., Lee K.J.;
RT "Characterization of the leupeptin-inactivating enzyme from
RT Streptomyces exfoliatus SMF13 which produces leupeptin.";

RL Biochem. J. 331:539-545(1998).
 CC -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN
 CC CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.
 CC OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.
 CC -!- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-
 CC LEUCINE, LEUCINE AND ARGININAL.
 CC -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1
 CC SITE.
 CC -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE
 CC INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 KW Hydrolase; Metalloprotease.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1373 MW; 14D627940C973260 CRC64;

 Query Match 32.3%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 5 LPVNV 10
 :|: ||
 Db 7 IPLANV 12

 RESULT 26
 Q8M099
 ID Q8M099 PRELIMINARY; PRT; 14 AA.
 AC Q8M099;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 6 (Fragment).
 OS Tockus nasutus (African grey hornbill).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Bucerotiformes; Bucerotidae; Tockus.
 OX NCBI_TaxID=118205;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22024936; PubMed=12029361;
 RA Delport W., Ferguson J.W.H., Bloomer P.;
 RT "Characterization and evolution of the mitochondrial DNA control
 RT region in hornbills (Bucerotiformes).";
 RL J. Mol. Evol. 54:794-806(2002).
 DR EMBL; AY027933; AAK31783.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1638 MW; DFAE115DFA724E29 CRC64;

 Query Match 32.3%; Score 20; DB 8; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.1e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVNVL 11
| || : ||
Db 6 FFLGLAFVL 14

RESULT 27

P82340

ID P82340 PRELIMINARY; PRT; 14 AA.
AC P82340;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC --!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC --!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KW Chloroplast; Thylakoid.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1505 MW; 2EABFAF980F3D7D7 CRC64;

Query Match 32.3%; Score 20; DB 10; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVNV 9
| |||:
Db 5 FQPVVD 10

RESULT 28

O68425

ID O68425 PRELIMINARY; PRT; 15 AA.
AC O68425;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98290710; PubMed=9625791;
RA Baumann L., Baumann P., Moran N.A.;
RT "News & notes: the endosymbiont (Buchnera) of the aphid diuraphis
noxia contains all the genes of the tryptophan biosynthetic pathway.";
RL Curr. Microbiol. 37:58-59(1998).
DR EMBL; AF038565; AAC27732.1; -.
KW Hypothetical protein.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1795 MW; 54A3D5B40D326E1E CRC64;

Query Match 32.3%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LFFF 5
| |||
Db 8 LLFF 12

RESULT 29
Q8XF44
ID Q8XF44 PRELIMINARY; PRT; 15 AA.
AC Q8XF44;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phe leader peptide (Hypothetical protein STM2666).
GN T2621 OR STM2666 OR STY2853A.
OS Salmonella typhi, and
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601, 602;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.

RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant *Salmonella*
RT *enterica* serovar *Typhi* CT18.";
RL *Nature* 413:848-852(2001).
DR EMBL; AE016842; AAO70192.1; -.
DR EMBL; AE008821; AAL21555.1; -.
DR EMBL; AL627276; CAD05845.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 15 AA; 1959 MW; CFE1598393ED35E0 CRC64;

Query Match 32.3%; Score 20; DB 16; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFFL 5
|||:
Db 10 FFFI 13

RESULT 30
Q9UWK4
ID Q9UWK4 PRELIMINARY; PRT; 16 AA.
AC Q9UWK4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 53 kDa tungsten containing formylmethanofuran dehydrogenase
DE (Fragment).
OS *Methanobacterium thermoautotrophicum*.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE.
RX MEDLINE=94213570; PubMed=8161283;
RA Bertram P.A., Schmitz R.A., Linder D., Thauer R.K.;
RT "Tungstate can substitute for molybdate in sustaining growth of
RT *Methanobacterium thermoautotrophicum*. Identification and
RT characterization of a tungsten isoenzyme of formylmethanofuran
RT dehydrogenase.";
RL *Arch. Microbiol.* 161:220-228(1994).
SQ SEQUENCE 16 AA; 1838 MW; 03AC8809D4685199 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 VVNVL 12

| ||:|
4 VKNVVP 9

RESULT 31

Q06800

ID Q06800 PRELIMINARY; PRT; 17 AA.
AC Q06800;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE N1780.
GN N1780.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96287653; PubMed=8686380;
RA Nasr F., Becam A.M., Herbert C.J.;
RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
RT 24 complete open reading frames: 18 correspond to new genes, one of
RT which encodes a protein similar to the human myotonic dystrophy
RT kinase.";
RL Yeast 12:169-175(1996).
DR EMBL; X92517; CAA63292.1; -.
SQ SEQUENCE 17 AA; 2139 MW; BD7E9AAFADF754AF CRC64;

Query Match 32.3%; Score 20; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFLP 6
:|||
Db 12 YFLP 15

RESULT 32

Q8M0A0

ID Q8M0A0 PRELIMINARY; PRT; 18 AA.
AC Q8M0A0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 6 (Fragment).
OS Tockus leucomelas.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Bucerotiformes; Bucerotidae; Tockus.
OX NCBI_TaxID=153645;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22024936; PubMed=12029361;
RA Delport W., Ferguson J.W.H., Bloomer P.;
RT "Characterization and evolution of the mitochondrial DNA control
RT region in hornbills (Bucerotiformes).";

RL J. Mol. Evol. 54:794-806(2002).
DR EMBL; AY027931; AAK31782.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1966 MW; FA7531A2FFAE115D CRC64;

Query Match 32.3%; Score 20; DB 8; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.4e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVNVL 11
||| : ||
Db 6 FFLGLAFVL 14

RESULT 33
P83532
ID P83532 PRELIMINARY; PRT; 8 AA.
AC P83532;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 15 KDA.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 756 MW; 69CDD452D1B772C8 CRC64;

Query Match 30.6%; Score 19; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 1e+06;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVNVL 11
:| || :
Db 2 VPTVNAV 8

RESULT 34
Q9GD36
ID Q9GD36 PRELIMINARY; PRT; 9 AA.
AC Q9GD36;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S16 (Fragment).
GN RPS16.
OS Juncus effusus (Soft rush).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.
OX NCBI_TaxID=13579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RAasmussen C.B., Chase M.W.;
RT "Coding and noncoding plastid DNA in palm systematics.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ404962; CAC17904.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LFFF 4
:|||
Db 6 VFFF 9

RESULT 35
Q9AIZ7
ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861 (2001).
DR EMBL; AF211132; AAK15377.1; -.

DR GO; GO:0004812; F:tRNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

 Query Match 30.6%; Score 19; DB 2; Length 11;
 Best Local Similarity 30.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 LFFFPLPVNV 10
 | |: ::|:
 Db 2 LNMFIIKILNL 11

 RESULT 36
 Q9GI96
 ID Q9GI96 PRELIMINARY; PRT; 12 AA.
 AC Q9GI96;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
 DE (Fragment).
 GN RBCS.
 OS Sargassum polycystum.
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
 OC Sargassum.
 OX NCBI_TaxID=127578;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=nep127;
 RA Phillips N.E.;
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
 RT (Fucales, Phaeophyceae).";
 RL Thesis (1998), University of Hawaii.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=nep127;
 RA Phillips N.E., Smith C.M., Morden C.W.;
 RT "Testing the systematics of the genus Sargassum (Fucales,
 RT Phaeophyceae) with the Rubisco operon.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF244344; AAF98114.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;

 Query Match 30.6%; Score 19; DB 8; Length 12;
 Best Local Similarity 80.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 FFFFLP 6
 | |||
 Db 8 FPFLP 12

RESULT 37

Q37071

ID Q37071 PRELIMINARY; PRT; 12 AA.
AC Q37071;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S12 (Fragment).
GN RPS12.
OS Petunia hybrida (Petunia).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89136067; PubMed=3224388;
RA Aldrich J., Cherney B.W., Williams C., Merlin E.;
RT "Sequence analysis of the junction of the large single copy region and
RT the large inverted repeat in the petunia chloroplast genome.";
RL Curr. Genet. 14:487-492(1988).
DR EMBL; M37322; AAB02424.1; --.
DR EMBL; M35955; AAA84551.1; --.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1415 MW; D4394390BA140452 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVNV 9
|: :||
Db 1 FVAIVN 6

RESULT 38

Q14462

ID Q14462 PRELIMINARY; PRT; 13 AA.
AC Q14462;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glycophorin St-a (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding

RT human glycophorin variant St-a: Similarity to the crossing-over point
RT in haptoglobin-related genes.";
RL J. Biol. Chem. 265:9259-9263(1990).
DR EMBL; M33507; AAA35942.1; -.
DR PIR; I70076; I70076.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1489 MW; 466C6DF642414767 CRC64;

Query Match 30.6%; Score 19; DB 4; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.6e+04;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
||:::
Db 6 LPIISL 11

RESULT 39
Q16007
ID Q16007 PRELIMINARY; PRT; 13 AA.
AC Q16007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Lysosomal acid beta-galactosidase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91369478; PubMed=1909871;
RA Morreau H., Bonten E., Zhou X.Y., d'Azzo A.;
RT "Organization of the gene encoding human lysosomal beta-
galactosidase.";
RL DNA Cell Biol. 10:495-504(1991).
DR EMBL; S59584; AAB19814.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1482 MW; D70DAEE928194412 CRC64;

Query Match 30.6%; Score 19; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 VVNVL 12
:| :||
Db 5 LVRIL 10

RESULT 40
Q9QVK6
ID Q9QVK6 PRELIMINARY; PRT; 13 AA.
AC Q9QVK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373341; PubMed=1832670;
RA Hoppner W., Beckert L., Buck F., Seitz H.J.;
RT "Is the p29 protein involved in the rapid regulation of
RT phosphoenolpyruvate carboxykinase (GTP)?";
RL J. Biol. Chem. 266:17257-17260(1991).
SQ SEQUENCE 13 AA; 1456 MW; 39099D8CBBA6D2D7 CRC64;

Query Match 30.6%; Score 19; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
||||
Db 5 LPVV 8

RESULT 41
Q9PXB5
ID Q9PXB5 PRELIMINARY; PRT; 13 AA.
AC Q9PXB5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 170 kDa DHBV pre-S region binding protein (Fragment).
OS Duck hepatitis B virus (DHBV).
OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
OX NCBI_TaxID=12639;
RN [1]
RP SEQUENCE.
RX MEDLINE=96013813; PubMed=7474130;
RA Tong S., Li J., Wands J.R.;
RT "Interaction between duck hepatitis B virus and a 170-kilodalton
RT cellular protein is mediated through a neutralizing epitope of the pre-
RT S region and occurs during viral infection.";
RL J. Virol. 69:7106-7112(1995).
SQ SEQUENCE 13 AA; 1397 MW; DC47BFE014BCD772 CRC64;

Query Match 30.6%; Score 19; DB 12; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.6e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVVA 9
:||:|
Db 6 VPVLM 10

RESULT 42
P82884
ID P82884 PRELIMINARY; PRT; 13 AA.
AC P82884;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Temporin-1CE.
OS Rana clamitans (green frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=145282;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=20283865; PubMed=10822101;
RA Halverson T., Basir Y.J., Knoop F.C., Conlon J.M.;
RT "Purification and characterization of antimicrobial peptides from the
RT skin of the North American green frog Rana clamitans.";
RL Peptides 21:469-476(2000).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- MASS SPECTROMETRY: MW=1461.0; MW_ERR=0.02; METHOD=ELECTROSPRAY.
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
DR GO; GO:0006805; P:xenobiotic metabolism; IEA.
KW Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1462 MW; CC18586B9DF931AD CRC64;

Query Match 30.6%; Score 19; DB 13; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FLPVVNL 11
|| : |
Db 1 FLPFLATL 8

RESULT 43
Q26100
ID Q26100 PRELIMINARY; PRT; 14 AA.
AC Q26100;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ppmsp-5 (Fragment).
GN PPMSP-5.
OS Pratylenchus penetrans (Root-lesion nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
OX NCBI_TaxID=45929;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maryland isolate;
RA Setterquist R.A., Smith G.K., Jones R., Fox G.E.;
RT "Diagnostic Probes Targeting the Major Sperm Protein Gene may be
RT Useful for the Molecular Identification of Nematodes.";
RL J. Nematol. 0:0-0(1996).
DR EMBL; U57830; AAB02263.1; -.

FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1775 MW; 18EB70A35334554B CRC64;

Query Match 30.6%; Score 19; DB 5; Length 14;
Best Local Similarity 14.3%; Pred. No. 1.7e+04;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVVN 9
::: ::|
Db 7 YYMKIIN 13

RESULT 44

Q9TWF5

ID Q9TWF5 PRELIMINARY; PRT; 15 AA.
AC Q9TWF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Valyl-tRNA synthetase (Fragment).
OS Artemia (brine shrimps).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae.
OX NCBI_TaxID=6660;
RN [1]
RP SEQUENCE.
RX MEDLINE=96061959; PubMed=7588756;
RA Brandsma M., Kerjan P., Dijk J., Janssen G.M., Moller W.;
RT "Valyl-tRNA synthetase from Artemia. Purification and association with
RT elongation factor 1.";
RL Eur. J. Biochem. 233:277-282 (1995).
SQ SEQUENCE 15 AA; 1766 MW; 4D5CD234B274B09E CRC64;

Query Match 30.6%; Score 19; DB 5; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LFFFILPVVNVL 12
:|| : ||
Db 2 VFFAQELTGXL 13

RESULT 45

Q9S8F1

ID Q9S8F1 PRELIMINARY; PRT; 15 AA.
AC Q9S8F1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.18) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]

RP SEQUENCE.
 RX MEDLINE=95322859; PubMed=7599527;
 RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
 RA Greenland A.J.;
 RT "Characterization of the safener-induced glutathione S-transferase
 isoform II from maize.";
 RL Planta 196:295-302(1995).
 DR GO; GO:0004364; F:glutathione transferase activity; IEA.
 SQ SEQUENCE 15 AA; 1530 MW; 2F105C48F7DD3A56 CRC64;

 Query Match 30.6%; Score 19; DB 10; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.8e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 FLPV 7
 |:|||
 Db 4 FMPV 7

 RESULT 46
 O30985
 ID O30985 PRELIMINARY; PRT; 16 AA.
 AC O30985;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative ammonia transporter (Fragment).
 GN AMTB.
 OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16PHC;
 RX MEDLINE=98389683; PubMed=9721307;
 RA Qian Y., Tabita F.R.;
 RT "Expression of glnB and a glnB-like gene (glnK) in a ribulose
 RT bisphosphate carboxylase/oxygenase-deficient mutant of Rhodobacter
 RT sphaeroides.";
 RL J. Bacteriol. 180:4644-4649(1998).
 DR EMBL; AF023909; AAC34723.1; -.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1812 MW; EDB859A962D6FEEA CRC64;

 Query Match 30.6%; Score 19; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 1.9e+04;
 Matches 5; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

 Qy 1 LFFFPLPVVNVL 12
 | ||: :|||
 Db 7 LVFFM----ILP 14

RESULT 47
 Q8VNS8
 ID Q8VNS8 PRELIMINARY; PRT; 16 AA.

AC Q8VNS8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CadC protein (Fragment).
GN CADC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=413/89-1;
RA Benkel P., Chakraborty T.;
RT "Genetic organisation and sequence of the LEE II locus in Shiga toxin-
producing Escherichia coli.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ277443; CAC81838.1; -.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1826 MW; 0D5EA97E0C676A12 CRC64;

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVVNV 10
|||
Db 4 PVVRV 8

RESULT 48
094554
ID 094554 PRELIMINARY; PRT; 16 AA.
AC 094554;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calmodulin kinase 2 (Fragment).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA Alemany V., Alique R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U57982; AAD09466.1; -.
DR PIR; T44936; T44936.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1846 MW; 4A673B1F4C3288D9 CRC64;

Query Match 30.6%; Score 19; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFLPVVN 9
|| || |
Db 10 FFTVVTN 16

RESULT 49
Q26101
ID Q26101 PRELIMINARY; PRT; 16 AA.
AC Q26101;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ppmsp-6 (Fragment).
GN PPMSP-6.
OS Pratylenchus penetrans (Root-lesion nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
OX NCBI_TaxID=45929;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maryland isolate;
RA Setterquist R.A., Smith G.K., Jones R., Fox G.E.;
RT "Diagnostic Probes Targeting the Major Sperm Protein Gene may be
Useful for the Molecular Identification of Nematodes.";
RL J. Nematol. 0:0-0(1996).
DR EMBL; U57831; AAB02264.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1929 MW; 1058EB70A3533410 CRC64;

Query Match 30.6%; Score 19; DB 5; Length 16;
Best Local Similarity 14.3%; Pred. No. 1.9e+04;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVVN 9
::: ::|
Db 8 YYMKIIN 14

RESULT 50
O19977
ID O19977 PRELIMINARY; PRT; 16 AA.
AC O19977;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Photosystem I subunit (Fragment).
GN PSAI.
OS Gossypium mustelinum (Cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34275;
RN [1]
RP SEQUENCE FROM N.A.

RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL; AF031584; AAC63566.2; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1730 MW; A3145FAEFB57841E CRC64; ..

Query Match 30.6%; Score 19; DB 8; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|:|:|
Db 11 FVPLV 15

Search completed: July 4, 2004, 04:45:33
Job time : 24.4179 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 4.1194 Seconds
(without alignments)
151.683 Million cell updates/sec

Title: US-09-641-802-4

Perfect score: 62

Sequence: 1 LFFF LPVV NVLP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	25	40.3	13	1	CRBL_VESMA	P17232 vespa manda
2	23	37.1	12	1	GRAR_RANRU	P40754 rana rugosa
3	23	37.1	13	1	CRBL_VESLE	P17235 vespula lew
4	23	37.1	13	1	CRBL_VESXA	P17234 vespa xanth
5	22	35.5	13	1	BLAC_STRGR	P81173 streptomyce
6	22	35.5	17	1	UP36_UPEMJ	P82043 uperoleia m
7	21	33.9	13	1	CRBL_VESAN	P17233 vespa anali
8	21	33.9	13	1	CRBL_VESCR	P01518 vespa crabr
9	21	33.9	13	1	CRBL_VESTR	P17231 vespa tropi
10	21	33.9	13	1	HPB9_RANES	P32416 rana escule
11	21	33.9	13	1	TEMA_RANTE	P56917 rana tempor
12	21	33.9	13	1	TEMF_RANTE	P56921 rana tempor
13	21	33.9	14	1	CRBL_VESOR	P17236 vespa orien
14	20	32.3	13	1	HPA1_RANES	P32415 rana escule
15	20	32.3	18	1	ALL2_CYDPO	P82153 cydia pomon
16	19	30.6	13	1	TEMF_RANTE	P56919 rana tempor
17	19	30.6	14	1	UC15_MAIZE	P80621 zea mays (m

18	19	30.6	15	1	UC17_MAIZE	P80623	zea mays (m
19	18	29.0	13	1	TEME_RANTE	P56920	rana tempor
20	18	29.0	14	1	LPF2_ECOLI	P06985	escherichia
21	18	29.0	15	1	ESTB_SCHGA	P81011	schizaphis
22	18	29.0	15	1	LPF_ECOLI	P03057	escherichia
23	18	29.0	15	1	UC29_MAIZE	P80635	zea mays (m
24	17	27.4	8	1	ALL6_CYDPO	P82157	cydia pomon
25	17	27.4	8	1	NPMB_BOVIN	P15507	bos taurus
26	17	27.4	9	1	NEUU_CAVPO	P34966	cavia porce
27	17	27.4	11	1	CX5B_CONAL	P58849	conus aulic
28	17	27.4	12	1	V25K_WSSV	P82004	white spot
29	17	27.4	13	1	TEJA_RANJA	P83307	rana japoni
30	17	27.4	15	1	CKX_WHEAT	P58763	triticum ae
31	17	27.4	17	1	BOL5_MEGPE	P07496	megabombus
32	17	27.4	18	1	FMF1_ECOLI	P20860	escherichia
33	16	25.8	11	1	TKND_RANCA	P22691	rana catesb
34	16	25.8	12	1	UN39_CLOPA	P81359	clostridium
35	16	25.8	12	1	YZPY_ECOLI	P17776	escherichia
36	16	25.8	13	1	CRBL_ICASP	P17237	icaria sp.
37	16	25.8	13	1	MP1_MICOC	P81532	microplitis
38	16	25.8	13	1	TEMC_RANTE	P56918	rana tempor
39	16	25.8	13	1	YPNP_PHOLU	P41122	photorhabdu
40	16	25.8	14	1	JAP1_RANJA	P83305	rana japoni
41	16	25.8	15	1	ALLS_MANSE	P42559	manduca sex
42	16	25.8	15	1	RM12_YEAST	P36522	saccharomyc
43	16	25.8	17	1	RM35_YEAST	P36530	saccharomyc
44	16	25.8	17	1	TPIS_PINPS	P81666	pinus pinas
45	16	25.8	18	1	LUXB_KRYAS	P18300	kryptophana
46	16	25.8	18	1	PA55_SHEEP	P83202	ovis aries
47	15	24.2	8	1	AKH_LIBAU	P25418	libellula a
48	15	24.2	9	1	PPK1_PERAM	P82691	periplaneta
49	15	24.2	10	1	APE_CAPGI	P80474	capnocytoph
50	15	24.2	10	1	ESTA_SCHGA	P81012	schizaphis
51	15	24.2	10	1	HTF1_ROMMI	P18110	romalea mic
52	15	24.2	10	1	UPA5_HUMAN	P30091	homo sapien
53	15	24.2	12	1	TM2A_METMA	P80652	methanosarc
54	15	24.2	13	1	CRTC_RANES	P31832	rana escule
55	15	24.2	13	1	FIBB_RABIT	P14478	oryctolagus
56	15	24.2	13	1	PEDI_HYDAT	P80578	hydra atten
57	15	24.2	14	1	PH1_PRUSE	P29263	prunus sero
58	15	24.2	15	1	CDN4_LITCE	P82076	litoria cae
59	15	24.2	15	1	CYSK_CLOPA	P81340	clostridium
60	15	24.2	15	1	IRBP_CRISP	P12665	cricetidae
61	15	24.2	15	1	PH3_PRUSE	P29265	prunus sero
62	15	24.2	15	1	UC08_MAIZE	P80614	zea mays (m
63	15	24.2	15	1	UC30_MAIZE	P80636	zea mays (m
64	15	24.2	15	1	UP01_METAN	P83440	metarhizium
65	15	24.2	16	1	FOR2_MYRGU	P81437	myrmecia gu
66	15	24.2	16	1	PH2_PRUSE	P29264	prunus sero
67	15	24.2	18	1	A2M_OCTVU	P30800	octopus vul
68	14	22.6	8	1	HTF1_PERAM	P04548	periplaneta
69	14	22.6	9	1	COXE_THUOB	P80975	thunnus obe
70	14	22.6	9	1	LMT3_LOCMI	P41489	locusta mig
71	14	22.6	10	1	GON1_CHEPR	P80677	chelyosoma
72	14	22.6	10	1	HTF_NAUCI	P10939	nauphoeta c
73	14	22.6	10	1	PAP1_PARMA	P81863	pardachirus
74	14	22.6	11	1	PVK1_PERAM	P41837	periplaneta

75	14	22.6	11	1	TIN4_HOPTI	P82654 hoplobatrac
76	14	22.6	12	1	NUDM_CANFA	P54713 canis famil
77	14	22.6	12	1	TIN2_HOPTI	P82652 hoplobatrac
78	14	22.6	12	1	TIN3_HOPTI	P82653 hoplobatrac
79	14	22.6	13	1	IDHA_CANFA	P54836 canis famil
80	14	22.6	14	1	ADFA_TENMO	P82965 tenebrio mo
81	14	22.6	14	1	LPER_BACLI	Q04303 bacillus li
82	14	22.6	15	1	CX1B_CONBE	P58624 conus betul
83	14	22.6	15	1	LEC1_PSOSC	P22582 psophocarpu
84	14	22.6	15	1	MILT_ONCKE	P81037 oncorhynchus
85	14	22.6	15	1	PA59_SHEEP	P83444 ovis aries
86	14	22.6	15	1	PC20_BRANA	P81096 brassica na
87	14	22.6	15	1	SAL1_ONCMY	P81369 oncorhynchus
88	14	22.6	16	1	FOR1_MYRGU	P81438 myrmecia gu
89	14	22.6	16	1	LPK1_LOCMI	P20404 locusta mig
90	14	22.6	18	1	CPAX_BOVIN	P22779 bos taurus
91	14	22.6	18	1	MU21_LITGE	P82068 litoria gen
92	14	22.6	18	1	PCG6_PACGO	P82419 pachycondyl
93	14	22.6	18	1	TOP1_KLEAE	P46155 klebsiella
94	13	21.0	7	1	PPH2_LYCES	P83379 lycopersico
95	13	21.0	8	1	CPD1_ENTFA	P13269 enterococcus
96	13	21.0	9	1	BUK_CLOPA	P81337 clostridium
97	13	21.0	9	1	MGMT_BOVIN	P29177 bos taurus
98	13	21.0	9	1	NEUX_HUMAN	P04277 homo sapien
99	13	21.0	9	1	ULAE_HUMAN	P31931 homo sapien
100	13	21.0	10	1	ANG1_BOTJA	Q10581 bothrops ja

ALIGNMENTS

RESULT 1

CRBL_VESMA

ID CRBL_VESMA STANDARD; PRT; 13 AA.
 AC P17232;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vespid chemotactic peptide M (VESCP-M).
 OS Vespa mandarinia (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7446;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
 RA Fujino M.;
 RL (In) Munekata E. (eds.);
 RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
 RL Osaka (1984).
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 KW Mast cell degranulation; Chemotaxis; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;

Query Match 40.3%; Score 25; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 FLPVVNVL 11
| | |:: |
Db 1 FLPIIGKL 8

RESULT 2

GRAR_RANRU

ID GRAR_RANRU STANDARD; PRT; 12 AA.
AC P40754;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Granuliberin-R.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=78062810; PubMed=589733;
RA Nakajima T., Yasuhara T.;
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog
(Rana rugosa) skin.";
RL Chem. Pharm. Bull. 25:2464-2465(1977).
RN [2]
RP SYNTHESIS.
RX MEDLINE=78189201; PubMed=657408;
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,
RA Koyama K., Yajima H.;
RT "Synthesis of the dodecapeptide amide corresponding to the entire
RT amino acid sequence of granuliberin-R, a new frog skin peptide from
RT Rana rugosa.";
RL Chem. Pharm. Bull. 26:1222-1230(1978).
CC -!- FUNCTION: Mast cell degranulating peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Mast cell degranulation; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FFFLPV 7
| | |:
Db 1 FGFLPI 6

RESULT 3

CRBL_VESLE

ID CRBL_VESLE STANDARD; PRT; 13 AA.
AC P17235;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide L (VESCP-L).
OS Vespula lewisii (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1384 MW; C850402B8819233D CRC64;

Query Match 37.1%; Score 23; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPII 5

RESULT 4
CRBL_VESXA
ID CRBL_VESXA STANDARD; PRT; 13 AA.
AC P17234;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide X (VESCP-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7448;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;
Query Match 37.1%; Score 23; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPII 5

RESULT 5
BLAC_STRGR
ID BLAC_STRGR STANDARD; PRT; 13 AA.
AC P81173;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6) (Fragment).
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL B-2682;
RX MEDLINE=98386507; PubMed=9720038;
RA Deak E., Szabo I., Kalmanczhelyi A., Gal Z., Barabas G.,
RA Panyige A.;
RT "Membrane-bound and extracellular beta-lactamase production with
RT developmental regulation in Streptomyces griseus NRRL B-2682.";
RL Microbiology 144:2169-2177(1998).
CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -!- SUBCELLULAR LOCATION: SECRETED AND MEMBRANE-BOUND.
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PROSITE; PS00146; BETA_LACTAMASE_A; PARTIAL.
KW Hydrolase; Antibiotic resistance; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1236 MW; 14C5129118D54760 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNV 10
:|: ||
Db 6 IPIANV 11

RESULT 6
UP36_UPEMJ
ID UP36_UPEMJ STANDARD; PRT; 17 AA.
AC P82043;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 3.6.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- FUNCTION: Shows antibacterial activity against B.cereus, L.lactis,
CC L.innocua, M.luteus, S.aureus, S.epidermidis and S.uberis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1826; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 17 17 AMIDATION.
SQ SEQUENCE 17 AA; 1778 MW; 784D8BB46263CA3D CRC64;

Query Match 35.5%; Score 22; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VVNVL 11
|||||
Db 9 VVNVL 13

RESULT 7
CRBL_VESAN
ID CRBL_VESAN STANDARD; PRT; 13 AA.
AC P17233;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide A (VESCP-A).
OS Vespa analis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7449;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1386 MW; C85554365DF9233D CRC64;
Query Match 33.9%; Score 21; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FLPVV 8
|||:
Db 1 FLPMI 5

RESULT 8
CRBL_VESCR
ID CRBL_VESCR STANDARD; PRT; 13 AA.
AC P01518;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Crabrolin.
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84289390; PubMed=6206053;
RA Argiolas A., Pisano J.J.;
RT "Isolation and characterization of two new peptides, mastoparan C and
RT crabrolin, from the venom of the European hornet, Vespa crabro.";
RL J. Biol. Chem. 259:10106-10111(1984).
RN [2]
RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
RX MEDLINE=97419326; PubMed=9273892;
RA Krishnakumari V., Nagaraj R.;
RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue
RT peptide from the venom of the European hornet, Vespa crabro, and its
RT analogs.";
RL J. Pept. Res. 50:88-93(1997).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils. Has antimicrobial and hemolytic activity.
DR PIR; A01781; JZVHP1.
KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 33.9%; Score 21; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FLPVV 8
|||:
Db 1 FLPLI 5

RESULT 9

CRBL_VESTR

ID CRBL_VESTR STANDARD; PRT; 13 AA.

AC P17231;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Vespid chemotactic peptide T (VESCP-T).

OS Vespa tropica (Hornet).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespa.

OX NCBI_TaxID=7450;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RA Yasuhara T., Nakajima T., Erspaer V.;

RL (In) Sakakibara S. (eds.);

RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,

RL Osaka (1983).

CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis of neutrophils.

KW Mast cell degranulation; Chemotaxis; Amidation.

FT MOD_RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 33.9%; Score 21; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 9.5e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPIL 5

RESULT 10

HPB9_RANES

ID HPB9_RANES STANDARD; PRT; 13 AA.

AC P32416;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hemolytic protein B9 (Fragment).

OS Rana esculenta (Edible frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8401;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90198965; PubMed=2317508;

RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,

RA Barra D., Bossa F.;

RT "Purification and characterization of bioactive peptides from skin extracts of Rana esculenta.";

RL Biochim. Biophys. Acta 1033:318-323(1990).

CC -!- FUNCTION: Shows hemolytic activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S09019; S09019.
 KW Amphibian defense peptide; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

 Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 FLPVV 8
 |||:
 Db 1 FLPLI 5

RESULT 11
 TEMA_RANTE
 ID TEMA_RANTE STANDARD PRT; 13 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin A.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

 Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 FLPVV 8
 |||:
 Db 1 FLPLI 5

RESULT 12
 TEMF_RANTE

ID TEMF_RANTE STANDARD; PRT; 13 AA.
 AC P56921;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin F.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: Has antibacterial activity against Gram-negative and
 CC Gram-positive bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

 Query Match 33.9%; Score 21; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 FLPVV 8
 |||:
 Db 1 FLPLI 5

RESULT 13
 CRBL_VESOR
 ID CRBL_VESOR STANDARD; PRT; 14 AA.
 AC P17236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histamine releasing peptide II (HR-II).
 OS Vespa orientalis (Oriental hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7447;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Miroshnikov A.I., Snejzhkova L.G., Nazimov I.V., Reshetova O.I.,
 RA Rozynov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 RT venom of Vespa orientalis hornet.";

RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
DR PIR; JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;

Query Match 33.9%; Score 21; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPLI 5

RESULT 14
HPA1_RANES
ID HPA1_RANES STANDARD PRT; 13 AA.
AC P32415;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein A1 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S09018; S09018.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 32.3%; Score 20; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FLPVV 8
|||:
Db 1 FLPAI 5

RESULT 15

ALL2_CYDPO
ID ALL2_CYDPO STANDARD; PRT; 18 AA.
AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiae statin 2.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2169 MW; 8E66679C0CDF175C CRC64;

Query Match 32.3%; Score 20; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVNV 9
 ||| |
Db 11 LPVYN 15

RESULT 16
TEMD_RANTE
ID TEMD_RANTE STANDARD; PRT; 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Temporin D.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has no antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Skin.
 CC --!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 3EF35DFA655B2448 CRC64;

 Query Match 30.6%; Score 19; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 Qy 5 LPVVNL 11
 ||:| |
 Db 2 LPIVGNL 8

RESULT 17
 UC15_MAIZE
 ID UC15_MAIZE STANDARD; PRT; 14 AA.
 AC P80621;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC --!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.8, its MW is: 35.7 kDa.
 DR Maize-2DPAGE; P80621; COLEOPTILE.
 DR MaizeDB; 123947; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

 Query Match 30.6%; Score 19; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPVV 8
 ||||
 Db 5 LPVV 8

RESULT 18
 UC17_MAIZE
 ID UC17_MAIZE STANDARD; PRT; 15 AA.

AC P80623;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 42.7 kDa.
 DR Maize-2DPAGE; P80623; COLEOPTILE.
 DR MaizeDB; 123949; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1554 MW; C0AFFF15FFECEEC8 CRC64;

 Query Match 30.6%; Score 19; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Qy 5 LPVVNVLP 12
 :|| || |
 Db 4 VPVFAVAP 11

 RESULT 19
 TEME_RANTE
 ID TEME_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin E.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).

CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVVNL 11
||:|
Db 2 LPIIGNL 8

RESULT 20
LPF2_ECOLI
ID LPF2_ECOLI STANDARD PRT; 14 AA.
AC P06985;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phenylalanyl-tRNA synthetase operon leader peptide (PheST attenuator
DE peptide).
GN PHEM OR PHTL OR B1715 OR C5495 OR Z2744 OR ECS2422 OR STY1774 OR T1217
GN OR SF1516 OR S4806.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7,
OS Salmonella typhi, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 601, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=85210878; PubMed=3158742;
RA Springer M., Mayaux J.-F., Fayat G., Plumbridge J.A., Graffe M.,
RA Blanquet S., Grunberg-Manago M.;
RT "Attenuation control of the Escherichia coli phenylalanyl-tRNA
RT synthetase operon.";
RL J. Mol. Biol. 181:467-478(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=84090239; PubMed=6317865;
RA Fayat G., Mayaux J.-F., Sacerdot C., Fromant M., Springer M.,
RA Grunberg-Manago M., Blanquet S.;
RT "Escherichia coli phenylalanyl-tRNA synthetase operon region.
RT Evidence for an attenuation mechanism. Identification of the gene for
RT the ribosomal protein L20.";
RL J. Mol. Biol. 171:239-261(1983).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=88163794; PubMed=3126825;
RA Springer M., Graffe M., Mayaux J.-F., Dardel F., Fayat G.,
RA Blanquet S., Grunberg-Manago M.;
RT "Open reading frames in the control regions of the phenylalanyl-tRNA
RT synthetase operon of *E. coli*.";
RL Biochimie 69:1065-1070(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic *Escherichia coli*.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant *Salmonella*
RT *enterica* serovar *Typhi* CT18.";
RL *Nature* 413:848-852(2001).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of *Salmonella enterica* serovar *Typhi* strains Ty2
RT and CT18.";
RL *J. Bacteriol.* 185:2330-2337(2003).
RN [10]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
RT through comparison with genomes of *Escherichia coli* K12 and O157.";
RL *Nucleic Acids Res.* 30:4432-4441(2002).
RN [11]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of *Shigella*
RT *flexneri* serotype 2a strain 2457T.";
RL *Infect. Immun.* 71:2775-2786(2003).
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CC -----
DR EMBL; M10423; AAA23961.1; -.
DR EMBL; V00291; CAA23563.1; -.
DR EMBL; M13251; AAA24333.1; -.
DR EMBL; AE000266; AAC74785.1; -.
DR EMBL; AE016761; AAN80571.1; -.
DR EMBL; AE005394; AAG56702.1; -.

DR EMBL; AP002558; BAB35845.1; -.
DR EMBL; AL627271; CAD02016.1; -.
DR EMBL; AE016838; AAO68872.1; -.
DR EMBL; AE015174; AAN43106.1; -.
DR EMBL; AE016983; AAP16996.1; -.
DR PIR; B85780; B85780.
DR PIR; F90931; F90931.
DR PIR; S11551; LFECFS.
DR EcoGene; EG11272; pheM.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1762 MW; 7D31C48E0060F0D4 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 8 FFF 10

RESULT 21
ESTB_SCHGA
ID ESTB_SCHGA STANDARD; PRT; 15 AA.
AC P81011;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Esterase 56 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
(Fragment).
OS Schizaphis graminum (Aphid).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
OX NCBI_TaxID=13262;
RN [1]
RP SEQUENCE.
RX MEDLINE=97468499; PubMed=9327586;
RA Siegfried B.D., Ono M., Swanson J.J.;
RT "Purification and characterization of a carboxylesterase associated
RT with organophosphate resistance in the greenbug, Schizaphis graminum
RT (Homoptera: Aphididae).";
RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR InterPro; IPR002018; CarbesteraseB.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1609 MW; 1208B2BCCC969482 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PVVNV 10
||| :
Db 2 PVVRI 6

RESULT 22
LPF_ECOLI
ID LPF_ECOLI STANDARD; PRT; 15 AA.
AC P03057;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phe leader peptide (Attenuator peptide).
GN PHEL OR PHEAE OR B2598 OR SF2658 OR S4807.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=79033820; PubMed=360214;
RA Zurawski G., Brown K., Killingly D., Yanofsky C.;
RT "Nucleotide sequence of the leader region of the phenylalanine operon
RT of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=91072346; PubMed=2254312;
RA Gavini N., Davidson B.E.;
RT "pheAo mutants of Escherichia coli have a defective pheA attenuator.";
RL J. Biol. Chem. 265:21532-21535(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).

RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF PHENYLALANINE.
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CC -----
DR EMBL; V00314; CAA23600.1; -.
DR EMBL; M10431; AAA24329.1; -.
DR EMBL; M58024; AAA62783.1; -.
DR EMBL; AE000346; AAC75647.1; -.
DR EMBL; AE015281; AAN44154.1; -.
DR EMBL; AE016987; AAP17979.1; -.
DR PIR; A03593; LFECF.
DR EcoGene; EG11271; pheL.
KW Leader peptide; Complete proteome.
SQ SEQUENCE 15 AA; 1924 MW; CFE14AE3BFF935E0 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FFF 4
|||
Db 6 FFF 8

RESULT 23
UC29_MAIZE
ID UC29_MAIZE STANDARD; PRT; 15 AA.
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]

RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 37.6 kDa.
 DR Maize-2DPAGE; P80635; COLEOPTILE.
 DR MaizeDB; 123960; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

 Query Match 29.0%; Score 18; DB 1; Length 15;
 Best Local Similarity 33.3%; Pred. No. 3.6e+03;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 LPVVNV 10
 :|:|:
 Db 7 IPLVDI 12

RESULT 24
 ALL6_CYDPO
 ID ALL6_CYDPO STANDARD; PRT; 8 AA.
 AC P82157;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiae statin 6.
 OS Cydia pomonella (Codling moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

 Query Match 27.4%; Score 17; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 5 LPVNV 9
 ||: |
 Db 1 LPLYN 5

RESULT 25

NPMB_BOVIN
ID NPMB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Morphine modulating neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: Modulates the action of morphine.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FFLP 6
| | |
Db 1 FLFQP 5

RESULT 26

NEUU_CAVPO
ID NEUU_CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (NmU-9).
GN NMU.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=90341105; PubMed=2381877;

RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
 RT "Isolation and microsequence analysis of a novel form of neuromedin U
 RT from guinea pig small intestine.";
 RL Peptides 11:613-617(1990).
 CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes
 CC selective vasoconstriction.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the NMU family.
 DR InterPro; IPR008199; NMU.
 DR Pfam; PF02070; NMU; 1.
 DR PROSITE; PS00967; NMU; 1.
 KW Amidation; Hormone.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

 Query Match 27.4%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 FFFLP 6
 | | |
 Db 3 FLFRP 7

RESULT 27
 CX5B_CONAL
 ID CX5B_CONAL STANDARD; PRT; 11 AA.
 AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins.";
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.

CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FFLPVV 8
| ||:
Db 1 FCCPVI 6

RESULT 28
V25K_WSSV
ID V25K_WSSV STANDARD PRT; 12 AA.
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polyprotein (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
virus.";
RL Arch. Virol. 145:263-274(2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.3e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFFPLVV 8
| | | ||
Db 3 LSFTLSVV 10

RESULT 29
TEJA_RANJA
ID TEJA_RANJA STANDARD PRT; 13 AA.
AC P83307;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Temporin-1Ja.
OS Rana japonica (Japanese reddish frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=21826910; PubMed=11835990;
 RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
 RT "Antimicrobial peptides with atypical structural features from the
 skin of the Japanese brown frog *Rana japonica*.";
 RL Peptides 23:419-425(2002).
 CC -!- FUNCTION: Antibacterial activity against the Gram-negative
 CC bacterium *E.coli* and the Gram-positive bacterium *S.aureus*.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 DR GO; GO:0008225; F:Gram-negative antibacterial peptide activity; IDA.
 DR GO; GO:0008224; F:Gram-positive antibacterial peptide activity; IDA.
 DR GO; GO:0016999; P:antibiotic metabolism; IDA.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1407 MW; 3EF713EA610A2448 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 4.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVVNL 11
 ||:| |
 Db 2 LPLVGNL 8

RESULT 30
 CKX_WHEAT
 ID CKX_WHEAT STANDARD PRT: 15 AA.
 AC P58763;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokinin dehydrogenase (EC 1.5.99.12) (CKO) (CKX) (Fragment).
 OS *Triticum aestivum* (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; *Triticum*.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=cv. Samantha;
 RX MEDLINE=21099312; PubMed=11168382;
 RA Galuszka P., Frebort I., Sebela M., Sauer P., Jacobsen S., Pec P.;
 RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
 degradation in cereals.";
 RL Eur. J. Biochem. 268:450-461(2001).
 CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
 CC substituted adenine derivatives that are plant hormones, where the
 CC substituent is an isopentenyl group. Substrate preference is 2-(2-

CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
CC zeatin riboside.
CC -!- CATALYTIC ACTIVITY: N(6)-dimethylallyladenine + electron acceptor
CC = adenine + 3-methylbut-2-enal + reduced electron acceptor +
CC H₂O.
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Might be located on membranes.
CC -!- MISCELLANEOUS: Optimal pH is 6.5.
KW Oxidoreductase; Flavoprotein; FAD.
FT UNSURE 1 1
FT UNSURE 13 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;

Query Match 27.4%; Score 17; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
|||
Db 1 FLP 3

RESULT 31
BOL5_MEGPE
ID BOL5_MEGPE STANDARD; PRT; 17 AA.
AC P07496;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin V.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; E22595; E22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1731 MW; B076C091571606A5 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VNVL 11
:|||

Db 1 INVL 4

RESULT 32
FMF1_ECOLI
ID FMF1_ECOLI STANDARD; PRT; 18 AA.
AC P20860;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE F7-1 fimbrial protein (F7-1 pilin) (P adhesin) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=89079313; PubMed=2562836;
RA Hoschuetzky H., Lottspeich F., Jann K.;
RT "Isolation and characterization of the alpha-galactosyl-1,4-beta-
galactosyl-specific adhesin (P adhesin) from fimbriated Escherichia
coli.";
RL Infect. Immun. 57:76-81(1989).
CC -!- FUNCTION: Fimbriae (also called pili), polar filaments radiating
CC from the surface of the bacterium to a length of 0.5-1.5
CC micrometers and numbering 100-300 per cell, enable bacteria to
CC colonize the epithelium of specific host organs.
CC -!- MISCELLANEOUS: This is an alpha-galactosyl-1,4-beta-galactosyl-
CC specific adhesin.
DR PIR; A30541; A30541.
KW Fimbria.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1956 MW; E9A44CDA6E2886B5 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 18;
Best Local Similarity 44.4%; Pred. No. 6.3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LFFF LPVNN 9
Db 5 VFYSLGNVN 13

RESULT 33
TKND_RANCA
ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin D (RTK D).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D61033; D61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 FFLPV 7
| : | :
Db 7 FYAPM 11

RESULT 34
UN39_CLOPA
ID UN39_CLOPA STANDARD; PRT; 12 AA.
AC P81359;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 39 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.4, ITS MW IS: 29.5 kDa.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; 940561E66BD2CB01 CRC64;
Query Match 25.8%; Score 16; DB 1; Length 12;
Best Local Similarity 30.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LFFF LPVVNV 10
: : |||:
Db 1 MIYSTE VVNM 10

RESULT 35
YZPY_ECOLI
ID YZPY_ECOLI STANDARD PRT; 12 AA.
AC P17776;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Hypothetical pyrE leader peptide.
GN PYRL OR PYRE-LP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85003588; PubMed=6207018;
RA Poulsen P., Bonekamp F., Jensen K.F.;
RT "Structure of the Escherichia coli pyrE operon and control of pyrE
expression by a UTP modulated intercistronic attenuation.";
RL EMBO J. 3:1783-1790(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83287414; PubMed=6349999;
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
RA Lundberg L.G.;
RT "Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA
in front of the protein-coding region.";
RL Eur. J. Biochem. 135:223-229(1983).
CC -!- CAUTION: This sequence, according to the EcoSeq database (K. Rudd)
CC is probably not a real protein; therefore this entry will probably
CC be deleted in future releases.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00781; -; NOT_ANNOTATED_CDS.
DR EMBL; V01578; -; NOT_ANNOTATED_CDS.
DR PIR; A30400; LFECPE.

KW Hypothetical protein.
SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;
Query Match 25.8%; Score 16; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 4 LFF 6

RESULT 36

CRBL_ICASP
ID CRBL_ICASP STANDARD PRT; 13 AA.
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotactic peptide (I-CP).
OS Icaria sp. (Ropalidian wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Icaria.
OX NCBI_TaxID=7495;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation,
RL Osaka (1985).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.9e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 3 FFPLPVNVNL 11
| |:: :|
Db 4 FLGPLLGLL 12

RESULT 37

MP1_MICOC
ID MP1_MICOC STANDARD PRT; 13 AA.
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MP1 protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
OC Braconidae; Microgastrinae; Microplitis.
OX NCBI_TaxID=99573;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RA Takahashi M., Quicke D.L.J.;
RL Submitted (OCT-1998) to Swiss-Prot.
CC -!- TISSUE SPECIFICITY: Salivary glands.
CC -!- DEVELOPMENTAL STAGE: LARVAL.
FT NON_CONS 10 11
SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PVVNVL 11
| || :
Db 7 PPVNYI 12

RESULT 38
TEMC_RANTE
ID TEMC_RANTE STANDARD; PRT; 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Temporin C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LPVVNL 11

||:|
Db 2 LPILGNL 8

RESULT 39
YPNP_PHOLU
ID YPNP_PHOLU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3'region (ORF3) (Fragment).
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photorhabdus sp.
RT strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
CC -----
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CC -----
DR EMBL; X76069; CAA53672.1; -.
KW Hypothetical protein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFL 5
Db 3 FFL 5

RESULT 40
JAP1_RANJA
ID JAP1_RANJA STANDARD; PRT; 14 AA.
AC P83305;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Japonicin-1.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=21826910; PubMed=11835990;
 RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
 RT "Antimicrobial peptides with atypical structural features from the
 skin of the Japanese brown frog *Rana japonica*.";
 RL Peptides 23:419-425(2002).
 CC -!-- FUNCTION: Antibacterial activity against the Gram-negative
 CC bacterium *E.coli* and the Gram-positive bacterium *S.aureus*.
 CC -!-- SUBCELLULAR LOCATION: Secreted.
 CC -!-- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!-- MASS SPECTROMETRY: MW=2715.4; METHOD=Electrospray.
 DR GO; GO:0008225; F:Gram-negative antibacterial peptide activity; IDA.
 DR GO; GO:0008224; F:Gram-positive antibacterial peptide activity; IDA.
 DR GO; GO:0016999; P:antibiotic metabolism; IDA.
 KW Amphibian defense peptide; Antibiotic.
 FT DISULFID 8 14 BY SIMILARITY.
 SQ SEQUENCE 14 AA; 1650 MW; C278625186DBE0B9 CRC64;

 Query Match 25.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 4 FLPV 7
 | |:
 Db 1 FFPI 4

RESULT 41
 ALLS_MANSE
 ID ALLS_MANSE STANDARD; PRT; 15 AA.
 AC P42559;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Allatostatin (Mas-AS).
 OS *Manduca sexta* (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
 OC Sphingidae; Sphinginae; *Manduca*.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=92052112; PubMed=1946359;
 RA Kramer S.J., Toschi A., Miller C.A., Kataoka H., Quistad G.B.,
 RA Li J.P., Carney R.L., Schooley D.A.;
 RT "Identification of an allatostatin from the tobacco hornworm *Manduca*
 sexta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
 CC -!-- FUNCTION: Strongly inhibits juvenile hormone biosynthesis in vitro
 CC by the corpora allata from fifth-stadium larvae and adult females.
 CC -!-- SIMILARITY: Belongs to the allatostatin family.
 DR PIR; A61612; A61612.

KW Neuropeptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 15 AA; 1908 MW; 1605B77CDEBC838E CRC64;
Query Match 25.8%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPV 7
:| |:
Db 8 YFNPI 12

RESULT 42
RM12_YEAST
ID RM12_YEAST STANDARD; PRT; 15 AA.
AC P36522;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L12 (YmL12) (Fragment).
GN MRPL12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR SGD; L0002687; MRPL12.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1851 MW; 74BCD9FEDDDDB3900 CRC64;
Query Match 25.8%; Score 16; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 7.8e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFLPVV 8
:|: |:
Db 5 YFVEVI 10

RESULT 43
RM35_YEAST
ID RM35_YEAST STANDARD; PRT; 17 AA.
AC P36530;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L35 (YmL35) (Fragment).
GN MRPL35.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria.";
 RL FEBS Lett. 284:51-56(1991).
 DR PIR; S17274; S17274.
 DR GermOnline; 140814; -.
 DR SGD; S0002730; MRPL35.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1826 MW; 6CE89CB415483EE8 CRC64;

 Query Match 25.8%; Score 16; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.8e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

 Qy 5 LPVVNVLP 12
 || || |
 Db 8 LPTDPVYP 15

RESULT 44
 TPIS_PINPS
 ID TPIS_PINPS STANDARD; PRT; 17 AA.
 AC P81666;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragments).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
 CC phosphate.
 CC -!- PATHWAY: Plays an important role in several metabolic pathways.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: In plants, there are two types of TPIS, cytosolic
 CC and plastid.

CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
 CC (spot N139) is: 5.9, its MW is: 24 kDa.
 CC -!- SIMILARITY: Belongs to the triosephosphate isomerase family.
 DR InterPro; IPR000652; Triophos_ismrse.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON_TER 1 1
 FT NON_CONS 9 10
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;

 Query Match 25.8%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 LFF 3
 |||
 Db 9 LFF 11

RESULT 45
 LUXB_KRYAS
 ID LUXB_KRYAS STANDARD; PRT; 18 AA.
 AC P18300;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase
 DE beta chain) (Fragment).
 GN LUXB.
 OS Kryptophanaron alfredi symbiont.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; light emitting symbionts of fish.
 OX NCBI_TaxID=28177;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91076680; PubMed=2256783;
 RA Haygood M.G.;
 RT "Relationship of the luminous bacterial symbiont of the Caribbean
 RT flashlight fish, Kryptophanaron alfredi (family Anomalopidae) to
 RT other luminous bacteria based on bacterial luciferase (luxA) genes.";
 RL Arch. Microbiol. 154:496-503(1990).
 CC -!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
 CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
 CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +
 CC light.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -----
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CC -----
DR EMBL; M36597; AAA91214.1; -.
DR InterPro; IPR002103; Bac_luciferase.
DR PROSITE; PS00494; BACTERIAL_LUCIFERASE; PARTIAL.
KW Photoprotein; Luminescence; Oxidoreductase; Monoxygenase;
KW Flavoprotein; FMN.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;

Query Match 25.8%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LFF 3
|||
Db 5 LFF 7

RESULT 46
PA55_SHEEP
ID PA55_SHEEP STANDARD; PRT; 18 AA.
AC P83202;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pregnancy-associated glycoprotein 55 (EC 3.4.23.-) (ovPAG-55)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amiri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to peptidase family A1.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; NAS.
DR GO; GO:0016787; F:hydrolase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001969; Aspprotease_AS.
DR PROSITE; PS00141; ASP_PROTEASE; PARTIAL.
KW Hydrolase; Aspartyl protease; Glycoprotein; Multigene family.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2128 MW; AA5F039CD95CA72A CRC64;

Query Match 25.8%; Score 16; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LPVVNV 10

||: |:
Db 8 LPLRNM 13

RESULT 47
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS *Libellula auripennis* (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 24.2%; Score 15; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 VNVL 12
|| |
Db 2 VNFTP 6

RESULT 48
PPK1_PERAM
ID PPK1_PERAM STANDARD; PRT; 9 AA.
AC P82691;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Pea-PK-1) (FXPRL-amide).
OS *Periplaneta americana* (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 24.2%; Score 15; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FLP 6
| : |
Db 5 FIP 7

RESULT 49
APE_CAPGI
ID APE_CAPGI STANDARD PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence

RT factor.";
 RL Microbiology 141:3087-3093 (1995).
 CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
 CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
 CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
 CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
 CC CAVITY.
 CC -!- COFACTOR: Requires magnesium or calcium.
 KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

 Query Match 24.2%; Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 VNVL 11
 ||:|
 Db 2 VNML 5

RESULT 50
 ESTA_SCHGA
 ID ESTA_SCHGA STANDARD; PRT; 10 AA.
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 DE (Fragment).
 OS Schizaphis graminum (Aphid).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
 OX NCBI_TaxID=13262;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated
 RT with organophosphate resistance in the greenbug, Schizaphis graminum
 RT (Homoptera: Aphididae).";
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro; IPR002018; CarbesteraseB.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KW Hydrolase; Serine esterase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

 Query Match 24.2%; Score 15; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 7.9e+03;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PVVN 9
|:|:
Db 2 PIVS 5

Search completed: July 4, 2004, 04:41:28
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